

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nontropic; neuroprotective;
 KW antiParkinsonian; antidiabetic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haemato poetic disorder; dyslipidaemia.
 XX OS Homo sapiens.
 XX WO2003029424-A2.
 XX PN 10-APR-2003.
 PD 02-OCT-2002; 2002WO-US031373.
 PF XX 02-OCT-2001; 2001US-0326493P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330399P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0343626P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-037385P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373B1P.
 PR 19-APR-2002; 2002US-0373B26P.
 PR 19-APR-2002; 2002US-0373854P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381031P.
 PR 16-MAY-2002; 2002US-038108B.
 PR 16-MAY-2002; 2002US-038108P.
 PR 28-MAY-2002; 2002US-0381612P.
 PR 29-MAY-2002; 2002US-0383616P.
 PR 01-OCT-2002; 2002US-0383831P.
 PR 01-OCT-2002; 2002US-039135P.
 XX PA (CURAGEN CORP.
 XX PI Milet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Pattrajin M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zethusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Perna CR, Shency SG;
 PI Shimkets RA, Robertberg ME, Leach MD, Agee ML, Berghs C, DiPippo VA;
 PI Eisen AU, Gangolli EA, Rieger DK, Spaderna SK;
 DR 2003-381626/36.
 DR N-FSDB; ADA05733.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidaemia, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1: Page 170; 586PP; English.

CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described, (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC binds to the polypeptide described above; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the

CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytotatic, nontropic, neuroprotective, antiParkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

CC Sequence 252 AA;

CC Query Match 100.0%; Score 40; DB 6; Length 252;
 CC Best Local Similarity 100.0%; Pred. No. 2,3;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 RLSSMMKRY 9
 CC Db 122 RLSSMMKRY 130

RESULT 7
 AAR67888
 ID AAR67888 standard; protein; 253 AA.
 XX ID AAR67888
 AC AAR67888;
 XX AC
 XX DT 25-MAR-2003 (revised)
 DT 09-AUG-1995 (first entry)

XX Human stratum corneum chymotrophic recombinant enzyme (SCCE).

DE DE
 XX ID AAR67888
 XX XX Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
 XX callosities; keratosis pilaris; ichthyoses; eczema.
 XX Homo sapiens.
 OS OS
 PN PN WO950651-A1.
 XX XX
 PD PD 05-JAN-1995.
 XX XX
 PF PF 20-TUN-1994;
 PR PR 18-TUN-1993;
 XX XX 93DK-00000725.
 PA PA (SYMB-) SYMBICOM AB.
 XX XX
 PI Egeland T, Hansson L;
 DR WPI: 1995-052088/07.
 DR N-PSDB; AAQ81203.
 XX PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
 PT related vectors, transformed cells and polypeptides, useful for treating
 PT skin disorders, e.g. acne or psoriasis, and for identification of
 PT specific inhibitors.

XX Disclosure; Page 97; 137pp; English.
 XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
 CC and skin care products, especially to treat and prevent acne, xeroderma,
 CC or other hyperkeratotic conditions (e.g. callusities or keratoses
 CC pilariis, ichthyoses, psoriasis, eczema, etc. It is produced
 CC recombinantly following mammal, insect, plant, or microorganism
 CC transformation with plasmid PS507. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX Sequence 253 AA;

Query Match 100.0%; Score 40; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
 Db 123 RLSSMVKKV 131

RESULT 9
 ID ABB84421 standard; peptide; 253 AA.
 ID ABB84421 standard; peptide; 253 AA.
 AC ABB84421;
 AC ABB84421;
 XX DT 08-NCV-2002 (first entry)
 XX DE Human SCCE protein N-terminal fragment SEQ ID 48.
 XX KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
 XX KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
 XX KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
 XX KW pruritus; atopic dermatitis; eczema; acne; itch; KIK7; enzyme.
 XX OS Homo sapiens.
 XX PN WO200262135-A2.
 XX PD 15-AUG-2002.
 XX PP 08-FEB-2002; 2002WO-IB001300.
 XX PR 09-FEB-2001; 2001CA-02332655.
 XX PR 09-FEB-2001; 2001DK-00000218.
 XX PA (EGELRD/) EGELRD T.
 XX PA (HANSEN/L) HANSEN L.
 XX PI Egelrud T, Hansson L;
 XX DR WPI; 2002-643380/69.

XX Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 XX Example 6; Page 37; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide sequence
 CC comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous gene
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathogenic condition, for development of testing of a
 CC cosmetic or a pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC inflammatory skin diseases selected from diseases consisting of epidermal
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful
 CC as a model for further studies of itch mechanisms and the testing of
 CC potential compounds and compositions for relieve of various skin diseases
 CC where itch is component. This sequence represents the N-terminal
 CC fragment of the human stratum corneum chymotryptic enzyme, SCCE
 CC synonymous with human kallikrein 7 (KLK7), used in the development of the
 CC transgenic mammals described in the invention

XX SQ Sequence 253 AA;
 XX Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer

XX

RESULT 12

ABU07440 standard; protein; 253 AA.

Qy 1 RLSSMVKV 9

XX ||||| |

DB 123 RLSSMVKV 131

AC ABU07440;

XX DT 28-JAN-2003 (first entry)

XX DE Protein differentially regulated in prostate cancer #43.

XX KW Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX OS Homo sapiens.

XX PN WO200281638-A2.

XX PD 17-OCT-2002.

XX PP 08-APR-2002; 2002WO-US010824.

XX PR 06-APR-2001; 2001US-0281731P.

PR 06-APR-2001; 2001US-0281732P.

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.

XX PI Sun Z, Jay G;

XX DR 2003-058520/05.

DR N-PSDB; ABX10343.

XX Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.

XX Claim 1; Page 293-294; 416pp; English.

XX The invention describes genes (I) which are differentially regulated in
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification

Sequence 253 AA:

Query Match 100.0%; Score 40; DB 6; Length 253;

Best Local Similarity 100.0%; Pred. No. 2.3%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

RESULT 13

ABU07471 standard; protein; 253 AA.

Qy 1 RLSSMVKV 9

DB 123 RLSSMVKV 131

AC ABU07471;

XX DT 28-JAN-2003 (first entry)

XX DE Protein differentially regulated in prostate cancer #74.

XX KW Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX OS Homo sapiens.

XX PN WO200281638-A2.

XX PD 17-OCT-2002.

XX PP 08-APR-2002; 2002WO-US010824.

XX PR 06-APR-2001; 2001US-0281731P.

PR 06-APR-2001; 2001US-0281732P.

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.

XX PI Sun Z, Jay G;

XX DR 2003-058520/05.

DR N-PSDB; ABX10343.

XX Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.

XX Claim 1; Page 351; 416pp; English.

XX The invention describes genes (I) which are differentially regulated in
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification

CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide; (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer

XX Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Gaps 0;
 Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

RESULT 14
 ABR58471 standard; protein; 253 AA.
 ID ABR58471
 XX
 AC ABR58471/
 XX
 DT 07-JUL-2003 (first entry)
 DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
 XX Human; Cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
 XX Homo sapiens.
 OS Homo sapiens.

XX WO200302468-A1.
 PN 10-APR-2003.
 PD 02-OCT-2002; 2002WO-US031467.
 PR 02-OCT-2001; 2001US-0327135P
 PR 30-MAY-2002; 2002US-0384531P
 XX (CORI-X CORIXA CORP.
 PA Algate PA, Mannion J;
 PI DR; 2003-372001/35.

XX New polynucleotide and polypeptide useful for diagnosing and/or treating
 PT cancer, particularly ovarian cancer, and as a vaccine.
 XX Claim 2; Page 157-158; 169pp; English.
 PS The invention relates to a novel isolated polynucleotide. The
 CC polynucleotides of the invention have cytostatic activity, and may have a
 CC use in gene therapy, and in a vaccine. The composition and methods are
 CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
 CC The composition may also be used as a vaccine to prevent cancer. The
 CC present sequence is used in the exemplification of the invention

XX Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Gaps 0;
 Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Gaps 0;
 Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

RESULT 15
 ADB80484 standard; protein; 253 AA.
 ID ADB80484
 XX
 AC ADB80484;
 XX
 DT 04-DEC-2003 (first entry)
 DE Ovarian cancer-associated protein #24.
 XX
 KW Cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
 KW post-operative chemotherapy; radiation therapy; tumour prognosis;
 KW pre-cancerous lesion detection.

XX Homo sapiens.
 OS Homo sapiens.
 XX WO200310235-A2.
 PN 27-DEC-2002.
 PD 18-JUN-2002; 2002WO-US019297.
 PR 18-JUN-2001; 2001US-0299234P.
 PR 27-AUG-2001; 2001US-031587P.
 PR 05-SEP-2001; 2001US-031744P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOS-) EOS BIOTECHNOLOGY INC.
 PA Mack DH, Gish RC;
 PI WPI; 2003-167431/16.
 DR N-PSDP; ADB80483.

XX Detecting an ovarian cancer-associated transcript in a cell from a
 PT biological sample from the patient with a
 PT polynucleotide that hybridizes to an ovarian cancer gene.

XX Claim 13; Page 291; 332pp; English.

XX The invention relates to a method of detecting an ovarian cancer-
 CC associated transcript in a cell from a patient, by contacting a
 CC biological sample from the patient with a polynucleotide that selectively
 CC hybridizes to a sequence at least 80% identical to any of one of 80
 CC nucleic acid sequences given in the specification. The method is useful
 CC in diagnosing ovarian cancer and in identifying and using agents and/or
 CC targets that inhibit ovarian cancer. The nucleic acid molecule,
 CC polypeptide and the antibody may also be used in detecting ovarian
 CC cancers, monitoring and early detection of relapse following treatment,
 CC chemotherapy or radiation therapy, selecting patients for post-operative
 CC determining tumour prognosis, early detection of pre-cancerous lesions,
 CC and as vaccines. This sequence corresponds to one of the proteins used
 CC for the detection method of the invention.

XX Sequence 253 AA;

Query Match 100.0%; Score 40; DB 7; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

Wed Mar 3 07:49:08 2004

us-09-905-083-32.rag

Page 10

Search completed: March 1, 2004, 17:28:47
Job time : 46.5556 secs

APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
 FILE REFERENCE: D6223CIP/C DIV
 CURRENT APPLICATION NUMBER: US/09/905,083
 PRIORITY FILING DATE: 2001-07-13
 PRIORITY APPLICATION NUMBER: US 09/502,600
 PRIORITY FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 32
 LENGTH:
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 123-131 of the SCCE protein
 US-09-905-083-32

Query Match 100.0%; Score 40; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 1 RLSSMVKV 9

RESULT 3
 US-09-796-294-4
 Sequence 4, Application US/09796294
 Patent No. US20020037581A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 ATTORNEY: Underwood, Lowell J.
 TITLE OF INVENTION: Extracellular Serine Protease
 FILE REFERENCE: D6020CIP3
 CURRENT APPLICATION NUMBER: US/09/796,294
 CURRENT FILING DATE: 2001-02-28
 PRIORITY APPLICATION NUMBER: US 09/618,259
 PRIORITY FILING DATE: 2000-07-18
 NUMBER OF SEQ ID NOS: 72
 SEQ ID NO: 4
 LENGTH: 144
 TYPE: PRT
 ORGANISM: unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
 OTHER INFORMATION: enzyme (scce) catalytic domain
 US-09-796-294-4

Query Match 100.0%; Score 40; DB 9; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 60 RLSSMVKV 68

RESULT 4
 US-10-461-787-4
 Sequence 4, Application US/10461787
 Publication No. US20030199010A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 ATTORNEY: Underwood, Lowell J.
 TITLE OF INVENTION: US20030199010A1 extracellular Serine Protease
 FILE REFERENCE: D6020CIP2
 CURRENT APPLICATION NUMBER: US/10/461,787
 CURRENT FILING DATE: 2003-06-13
 PRIORITY APPLICATION NUMBER: US/09/618,259
 PRIORITY FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: US 09/127,444
 PRIORITY FILING DATE: 1998-08-21
 NUMBER OF SEQ ID NOS: 72
 SEQ ID NO: 4
 LENGTH: 144
 TYPE: PRT
 ORGANISM: unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
 OTHER INFORMATION: enzyme (scce) catalytic domain
 US-10-461-787-4

Query Match 100.0%; Score 40; DB 14; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 60 RLSSMVKV 68

RESULT 5
 US-09-888-615-98
 Sequence 98, Application US/09888615
 Patent No. US20020064855A1
 GENERAL INFORMATION:
 APPLICANT: BLOOMMAN, GREGORY
 ATTORNEY: WHITE, DAVID
 APPLICANT: CAENEBEL, SEAN
 ATTORNEY: CHARVOZAK, GLEN
 APPLICANT: MANNING, GERARD
 APPLICANT: SUDARANAN, SUCHA
 TITLE OF INVENTION: NOVEL PROTEASES
 FILE REFERENCE: 098602/1214
 CURRENT APPLICATION NUMBER: US/09/888,615
 CURRENT FILING DATE: 2001-06-26
 PRIORITY APPLICATION NUMBER: 60/214,047
 PRIORITY FILING DATE: 2000-06-26
 NUMBER OF SEQ ID NOS: 150
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO: 98
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-888-615-98

Query Match 100.0%; Score 40; DB 9; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

RESULT 6
 US-09-764-762-3
 Sequence 3, Application US/09764762
 Patent No. US2002006834A1
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 ATTORNEY: Hall, Brett
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Incyte Pharmaceuticals, Inc.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 CURRENT APPLICATION DATA: Farsereo for Windows Version 2.0
 APPLICATION NUMBER: US/09/764,762
 FILING DATE: 16-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0252 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-1166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 532504
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-764-762-3

Query Match 100.0%; Score 40; DB 9; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMYKRV 9
 Db 123 RLSSMYKRV 131

RESULT 7
 US-10-264-283-90
 Sequence 90 Application US/10244283
 Publication No. US20030144194A1
 GENERAL INFORMATION:
 APPLICANT: Algare, Paul A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 FILE REFERENCE: 210111.590
 CURRENT APPLICATION NUMBER: US/10/264,283
 CURRENT FILING DATE: 2002-10-02
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: Corixa Invention Disclosure Database
 SEQ ID NO 90
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match 100.0%; Score 40; DB 14; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMYKRV 9
 Db 123 RLSSMYKRV 131

RESULT 8
 US-10-295-027-498
 Sequence 498 Application US/10295027
 Publication No. US2003023250A1
 GENERAL INFORMATION:

APPLICANT: Afar, Daniel
 APPLICANT: Aziz, Natasha
 APPLICANT: Ginsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevesi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer Compositions and Screening For Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: Patent-in Ver. 2.1
 SEQ ID NO 498
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-127-498

Query Match 100.0%; Score 40; DB 15; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMYKRV 9
 Db 123 RLSSMYKRV 131

RESULT 9
 US-10-173-999-48
 Sequence 48 Application US/10173999
 Publication No. US20040005563A1
 GENERAL INFORMATION:
 APPLICANT: Mack, David H.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer Compositions and Methods of Screening for Modulators of Ovarian
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 018501-002420US
 CURRENT APPLICATION NUMBER: US/10/173,999
 CURRENT FILING DATE: 2002-06-17
 PRIOR APPLICATION NUMBER: US 60/299,234
 PRIOR FILING DATE: 2001-06-18
 PRIOR APPLICATION NUMBER: US 60/315,287
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13

US-09-905-083-110
 PRIORITY APPLICATION NUMBER: US 60/372,246
 PRIOR FILING DATE: 2001-04-12
 NUMBER OF SEQ ID NOS: 163
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 48
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-173-999-48

Query Match 100.0%; Score 40; DB 15; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7%;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 US-10-094-240-4
 Query Match 90.0%; Score 36; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RLSSMVKK 8
 Db 2 RLSSMVKK 9

GENERAL INFORMATION:
 APPLICANT: ZWIEBEL, LAURENCE J.
 TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
 FILE REFERENCE: N8289
 CURRENT APPLICATION NUMBER: US/10/094,240
 CURRENT FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: 10/056,405
 PRIOR FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: 60/264,649
 PRIOR FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4
 TYPE: PRT
 ORGANISM: Anopheles gambiae
 US-10-094-240-4

RESULT 10
 US-09-918-243-110
 Sequence 110, Application US/09918243
 Patient No. US20020142317A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Cannon, Martin J.
 APPLICANT: Santini, Alessandro
 TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D62223CIP/CID/CIP
 CURRENT APPLICATION NUMBER: US/09/918,243
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: US
 PRIOR FILING DATE: 2001-07-13
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 110
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 122-130 of the SCCE protein
 US-09-918-243-110

RESULT 13
 US-10-094-240-4
 Query Match 82.5%; Score 33; DB 14; Length 394;
 Best Local Similarity 77.8%; Pred. No. 80;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLSSMVKV 9
 Db 207 RLGSMVKL 215

GENERAL INFORMATION:
 APPLICANT: ZWIEBEL, LAURENCE J.
 TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF USE THEREOF
 FILE REFERENCE: N7841
 CURRENT APPLICATION NUMBER: US/10/056,405
 CURRENT FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: 60/264,649
 PRIOR FILING DATE: 2001-01-26
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4
 LENGTH: 394
 TYPE: PRT
 ORGANISM: Anopheles gambiae
 US-10-094-240-4

RESULT 11
 US-09-905-083-110
 Sequence 110, Application US/09905083
 Patient No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 TITLE OF INVENTION: Ovarian Cancer
 FILE REFERENCE: D6223CIP/CID/CIP
 CURRENT APPLICATION NUMBER: US/09/905,083
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US/09/502,600
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 110
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-094-240-4

RESULT 10
 US-10-094-240-4
 Query Match 82.5%; Score 33; DB 14; Length 394;
 Best Local Similarity 77.8%; Pred. No. 80;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLSSMVK 9
 Db 207 RLGSMVKL 215

US-09-918-243-79
 / Sequence 79; Application US/09918243
 / GENERAL INFORMATION:
 / APPLICANT: O'Brien, Timothy J.
 / APPLICANT: Cannon, Martin J.
 / APPLICANT: Santin, Alessandro
 / TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 / CURRENT APPLICATION NUMBER: US/09/918,243
 / FILE REFERENCE: D6223CIP/C/D/CP
 / CURRENT FILING DATE: 2001-07-30
 / PRIOR APPLICATION NUMBER: US
 / PRIOR FILING DATE: 2001-07-13
 / NUMBER OF SEQ ID NOS: 136
 / SEQ ID NO 79
 / LENGTH: 9
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CHAIN
 / OTHER INFORMATION: Residues 125-133 of the SCCE protein

US-09-918-243-79
 Query Match 77.5%; Score 31; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No 7.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SSMVKKV 9
 Db 1 SSMVKKV 7

RESULT 15
 US-09-918-243-87
 / Sequence 87; Application US/09918243
 / Patent No. US2002142317A1
 / GENERAL INFORMATION:
 / APPLICANT: O'Brien, Timothy J.
 / APPLICANT: Cannon, Martin J.
 / APPLICANT: Santin, Alessandro
 / TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 / CURRENT APPLICATION NUMBER: US/09/918,243
 / CURRENT FILING DATE: 2001-07-30
 / PRIOR APPLICATION NUMBER: US
 / PRIOR FILING DATE: 2001-07-13
 / NUMBER OF SEQ ID NOS: 136
 / SEQ ID NO 87
 / LENGTH: 9
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CHAIN
 / OTHER INFORMATION: Residues 125-133 of the SCCE protein

US-09-918-243-87
 Query Match 77.5%; Score 31; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No 7.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 SSMVKKV 9
 Db 1 SSMVKKV 7

Search completed: March 1, 2004, 18:08:49
 Job time : 25.1111 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode

Run on: March 1, 2004, 17:21:01 ; Search time 10.2222 Seconds
(without alignments)
84.690 Million cell updates/sec

Title: US-09-905-083-32
Perfect score: 40
Sequence: 1 RLSSWYTKV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.4

1: Piri;*
2: Piri;*
3: Piri;*
4: Piri;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	253	2 A53968	serine protease SCCE precursor - human
2	33	82.5	282	2 T135294	N/Alternate names: stratum corneum chymotryptic enzyme
3	33	82.5	372	2 S20056	C/Species: Homo sapiens (man)
4	33	82.5	560	2 S50401	C/Accession: A53968
5	32	80.0	350	1 C70009	R/Hansson, L.; Stromgqvist, M.; Baekman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
6	32	80.0	351	2 D90264	J. Biol. Chem. 269, 19420-19426, 1994
7	32	80.0	358	2 T38914	A/Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
8	32	80.0	589	2 A71277	A/Reference number: A53968; PMID: 8034709
9	32	80.0	664	2 T50316	A/Accession: A53968
10	31	77.5	912	2 H85470	A/Molecule type: mRNA
11	31	77.5	925	2 T05012	A/Cross-references: GDB:PRSS6; SCCE
12	30	75.0	239	2 T02473	A/Genes: GDB:PRSS6; SCCE
13	30	75.0	240	2 T13236	A/Cross-references: GDB:177730
14	30	75.0	318	2 T56519	A/Map Position: 7q31-7q35
15	30	75.0	319	2 JC5402	C/Genetics: F30-245/Domain: trypsin homology <TRY>
16	30	75.0	373	2 G5073	C/Suprafamily: trypsin; trypsin homology
17	30	75.0	457	2 D85429	F/30-245/Domain: trypsin homology <TRY>
18	30	75.0	532	2 T01759	Qy 1 RLSSWYTKV 9
19	30	75.0	647	2 A49218	Db 123 RLSSWYTKV 131
20	30	75.0	833	2 A47528	RESULT 2
21	30	75.0	986	2 E90220	Probable endo alpha-1,4 polygalactosaminidase - <i>Streptomyces coelicolor</i>
22	30	75.0	1167	2 A82543	C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
23	30	75.0	1846	2 T33079	R/Accession: T135294
24	29	72.5	253	2 JC5511	R/Seger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
25	29	72.5	285	2 A97255	A/Submitted to the EMBL Data Library, July 1999
26	29	72.5	336	2 E69214	A/Reference number: Z21574
27	29	72.5	337	2 AH2591	A/Accession: T135294
28	29	72.5	337	2 B97374	A/Status: preliminary; translated from GB/EMBL/DBJ
29	29	72.5	345	2 F90194	A/Molecule type: tRNA

RESULT 1

A53968

Serine protease SCCE precursor - human

N/

stratum corneum chymotryptic enzyme

C/

Species: Homo sapiens (man)

C/Accession: A53968

R/Hansson, L.; Stromgqvist, M.; Baekman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.

J. Biol. Chem. 269, 19420-19426, 1994

A/Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme

A/Reference number: A53968; PMID: 8034709

A/Accession: A53968

A/Molecule type: mRNA

A/Cross-references: GDB:177730

A/Genes: GDB:PRSS6; SCCE

A/Cross-references: GDB:177730

A/Map Position: 7q31-7q35

C/Genetics:

F/30-245/Domain: trypsin homology <TRY>

Query Match 100.0%

Best Local Similarity 100.0%

Mismatches 0;

Indels 0;

Gaps 0;

RESULT 2

T335294

Probable endo alpha-1,4 polygalactosaminidase - *Streptomyces coelicolor*

C/

Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

R/Accession: T135294

R/Seger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

A/Submitted to the EMBL Data Library, July 1999

A/Reference number: Z21574

A/Accession: T135294

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: tRNA

A/Residues: 1-282 <SEE>

A/Cross-references: EMBL:AL096872; PIDN:CAB51262.1; PMID:94306225; SCOEDB:SC55F7.23C

A/Experimental source: strain A3(2)

C/Genetics:

A/Genes: SCOEDB:SC55F7.23C

A/Cross-references:

Query Match 82.5%

Best Local Similarity 87.5%

Pred. No. 13;

Length 282;

Alignment

Qy	1 RLSSMVKV 8	Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Qy 1 RLSSMVKV 9 Db 347 RLKTMVKV 355
Db	265 RLSSMLKK 272		
		RESULT 5	
C70009	ABC transporter (lipoprotein) homolog yufN - <i>Bacillus subtilis</i>		
C;Species: <i>Bacillus subtilis</i>	par-hydroxybenzoate polyphenyltransferase (EC 2.5.1.-) precursor - yeast (Saccharomyces cerevisiae)		
C;Accession: C70009	Alternate names: 4-hydroxybenzoate hexapeptidyl transferase; protein N3119; protein YNR044C; Species: <i>Saccharomyces cerevisiae</i>		
C;Date: 10-Sep-1999	#sequence_revision 23-Apr-1993 #text_change 21-Jul-2000		
C;DB: 23-Apr-1993			
C;ID: S20056; S6372; JC2317			
C;Accession: S20056; MUID:9215658; PMID:1740455			
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Galizzi, A.; Galleni, R.; Hsiao, J.; Harwood, C.R.; Henaut, A.; Hilbertz, P.; Hocono, S.; Hollig, M.F.; Koetter, P.; Koningschein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Matuda, S.; Mauel, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scandalios, J.; Schleicher, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Seror, A.; Togoni, A.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yasuno, K.; Yata, K.; Yoshikawa, H.; Danchin, A.			
A;Cross-references: EMBL:MB1698; PID:gi171252; PID:AAA34507.1; PID:gi171254			
R;Pohl, T.M.	submitted to the Protein Sequence Database, April 1996		
A;Reference number: S63346			
A;Accession: S63372			
A;Molecule type: DNA			
A;Residues: 1-372 <ASH>			
A;Cross-references: EMBL:Z71654; PID:gi1302546; PID:e239832; PID:gi1302547; MIPS:INR041C			
A;Experimental source: strain S288C			
C;Genetics:			
A;Gene: SGD:COQ2			
A;Cross-references: SGD:S0005324; MIPS:YNR041C			
A;Map Position: 14R			
C;Keywords: isoprenoid biosynthesis; mitochondrion; transFerage; transmembrane protein			
F;1-22/Domain: transit peptide (mitochondrion) #status predicted <TRP>			
F;117-133/Domain: transmembrane #status Predicted <TM>			
F;172-188/Domain: transmembrane #status Predicted <TM>			
F;203-225/Region: polyphenyl diphosphate binding #status predicted			
Query Match Score 33; DB 2; Length 372; Best Local Similarity 77.8%; Pred. No. 17; Mismatches 1; Conservative 1; Indels 0; Gaps 0;			
Qy 1 RLSSMVKV 9 Db 326 RLFSMVKV 334		RESULT 6	
D90264	biorin synthase (biob) (imported) - <i>Sulfolobus solfataricus</i>		
C;Species: <i>Sulfolobus solfataricus</i>			
C;Accession: D90264			
C;DB: 24-May-2001	#sequence_revision 24-May-2001 #text_change 24-May-2001		
C;ID: 1-350			
C;Residues: 1-350 <XCN>			
A;Cross-references: GB:Z99120; GB:AL009126; PID:92635613; PIDN:CAB15143.1; PID:92635650			
A;Experimental source: strain 168			
C;Genetics:			
A;Gene: yufN			
C;Superfamily: ABC transporter_yufN			
A;Accession: C70009			
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-350 <XCN>			
A;Cross-references: GB:Z99120; GB:AL009126; PID:92635613; PIDN:CAB15143.1; PID:92635650			
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A;Status: Preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-350 <XCN>			
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A;Accession: D90264			
A;Status: Preliminary			
A;Molecule type: DNA			
A;Residues: 1-350 <XCN>			
A;Cross-references: GB:AE006641; PID:913814305; PIDN:AAK41371.1; GSPDB:GN00155			
A;Description: <i>Sulfolobus solfataricus</i> complete genome.			
A;Genetics:			
A;Gene: biob			
Query Match Score 32; DB 2; Length 351; Best Local Similarity 66.7%; Pred. No. 27; Mismatches 2; Conservative 6; Indels 0; Gaps 0;			
Qy 1 RLSSMVKV 9 Db 341 RLDSPLKKV 349			
D90264	biorin synthase (biob) (imported) - <i>Sulfolobus solfataricus</i>		
C;Species: <i>Sulfolobus solfataricus</i>			
C;Accession: D90264			
C;DB: 24-May-2001	#sequence_revision 24-May-2001 #text_change 24-May-2001		
C;ID: 1-350			
C;Residues: 1-350 <XCN>			
A;Cross-references: GB:Z99120; GB:AL009126; PID:92635613; PIDN:CAB15143.1; PID:92635650			
A;Experimental source: strain 168			
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A;Accession: D90264			
A;Status: Preliminary			
A;Molecule type: DNA			
A;Residues: 1-350 <XCN>			
A;Cross-references: GB:AE006641; PID:913814305; PIDN:AAK41371.1; GSPDB:GN00155			
A;Description: <i>Sulfolobus solfataricus</i> complete genome.			
A;Genetics:			
A;Gene: biob			
Query Match Score 32; DB 2; Length 351; Best Local Similarity 66.7%; Pred. No. 27; Mismatches 2; Conservative 6; Indels 0; Gaps 0;			
Qy 1 RLSSMVKV 9 Db 341 RLDSPLKKV 349			
D90264	biorin synthase (biob) (imported) - <i>Sulfolobus solfataricus</i>		
C;Species: <i>Sulfolobus solfataricus</i>			
C;Accession: D90264			
C;DB: 24-May-2001	#sequence_revision 24-May-2001 #text_change 24-May-2001		
C;ID: 1-350			
C;Residues: 1-350 <XCN>			
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A;Status: Preliminary			
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A;Status: Preliminary			
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A;Status: Preliminary			
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A;Experimental source: strain 168			
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A;Accession: D90264			
A;Status: Preliminary			
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A;Experimental source: strain 168			
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A;Status: Preliminary			
A;Molecule type: DNA			
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A;Cross-references: GB:Z99120; GB:AL009126; PID:92635613; PIDN:CAB15143.1; PID:92635650			
A;Experimental source: strain 168			
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A;Accession: D90264			
A;Status: Preliminary			
A;Molecule type: DNA			
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A;Experimental source: strain 168			
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A;Status: Preliminary			
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RESULT 7
T38914 para-hydroxybenzoate-polyprenyltransferase (BC 2.5.1.-) precursor, mitochondrial - fission
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38914
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21817
A;Accession: T38914
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
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A;Experimental source: strain 972h(-); cosmid c1703
C;Genetics:
A;Gene: SPDB:SPBC1703_03C
A;Map Position: 2
A;Introns: 43/3

Query Match	Score 32;	DB 2;	Length 664;
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Matches	Pred. No. 50;	Best Local Similarity	66.7%;
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	Indels 0;	Mismatches 1;	Gaps 0;

Qy 1 RLSMMYKRV 9
Db 624 RLXNMVTKI 632

RESULT 8
A;Accession: T769778
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A;Experimental source: strain 972h(-); cosmid C56F8
A;Gene: SPDB:SPAC56F8_04C
A;Map position: 1
A;Genotype: nuclear
C;Keywords: mitochondrial; transferase
A;Residues: 1-942 <SP0>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: H85470
C;Genetics:
A;Gene: ARG39750
A;Map Position: 4

Query Match	Score 31;	DB 2;	Length 912;
Best Local Similarity	77.5%;	Score 31;	DB 2;
Matches	Pred. No. 1.1e+02;	Best Local Similarity	55.6%;
	Mismatches 3;	Matches 5;	Conservative 3;
	Indels 0;	Mismatches 1;	Gaps 0;

Qy 1 RLSMMYKRV 9
Db 403 RESSMIRKI 411

RESULT 9
T50316 hypothetical Armadillo/beta-catenin domain protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50316
R;McHouggall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, F.
A;Reference number: Z225061
A;Reference number: 225061
A;Accession: T19P19_140
A;Cross-references: EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
C;Genetics:
A;Map Position: 4

Query Match	Score 31;	DB 2;	Length 925;
Best Local Similarity	77.5%;	Score 31;	DB 2;
Matches	Pred. No. 1.2e+02;	Best Local Similarity	55.6%;
	Mismatches 3;	Matches 5;	Conservative 2;
	Indels 0;	Mismatches 1;	Gaps 0;

Qy 1 RLSMMYKRV 9
Db 473 RISSLUKRV 481

Db 416 RFSSMIRKI 424

RESULT 12
 T02473 hypothetical protein At2g45740 [imported] - Arabidopsis thaliana
 N; Alternate names: hypothetical Protein F4I18.28
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
 C; Accession: T02473; C8894
 R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, A.; Description: Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence.
 A; Reference number: A84474
 A; Accession: T02473
 A; Status: translated from GB/EMBL/DBJU
 A; Molecule type: DNA
 A; Residues: 1-239 <R03>
 A; Cross-references: EMBL:AC004665; PID:G3386593; PID:g3386621
 A; Experimental source: cultivar Columbia
 R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; vanAken, S.E.; Umeyam, L.; Tallon, J.; Neierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999
 A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A; Reference number: A84420; MUID:20083487; PMID:1061797
 A; Accession: C84894
 A; Status: preliminary
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 A; Gene: At2g45740; F4I18.28
 A; Map position: 2
 A; Introns: 65/3; 90/3; 115/3; 142/3; 167/3
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 Best Local Similarity 66.7%; Pred. No. 53; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 148 RLSSSMKKI 156

RESULT 13
 T32363 hypothetical protein C08E3.12 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C; Accession: T32363
 R; Miller, N.; Kramer, J.; Kepler, D.
 A; Description: The sequence of *C. elegans* cosmid C08E3.
 A; Reference number: Z2115
 A; Accession: T32363
 A; Status: preliminary; translated from GB/EMBL/DBJU
 A; Molecule type: DNA
 A; Residues: 1-240 <ML>
 A; Cross-references: EMBL:AF025457; PID: AAB70970-1; GSPDB:GN00020; CESP:C08E3.12
 A; Experimental source: strain Bristol N2; clone C08E3
 C; Genetics:
 A; Gene: CESP:C08E3.12
 A; Map position: 2
 A; Introns: 167/3
 Query Match 75.0%; Score 30; DB 2; Length 240;
 Best Local Similarity 66.7%; Pred. No. 53; Indels 1; Gaps 0;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 193 RPSMLRKV 201

Search completed: March 1, 2004, 17:36:26
 Job time : 12.3333 secs

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Gapop 10.0 , Gapext 0.5			STANDARD; PRT; 253 AA.			
Total number of hits satisfying chosen parameters:					141681	
Minimum DB seq length: 0					Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%					Listing first 45 summaries	
Database :					Swissprot_42 : *	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query	Match Length	DB ID	Description	
1	40	100.0	253	1 KLK7_HUMAN	P49862 homo sapien	
2	33	82.5	372	1 COQ2_YEAST	P32378 saccharomyces	
3	33	82.5	560	1 YM23_YEAST	005452 bacillus subtilis	
4	32	80.0	350	1 YUN1_BACSU	Q10552 schizosaccharomyces pombe	
5	32	80.0	358	1 COQ2_SCOP0	08303 treponema pallidum	
6	7	32	80.0	589	1 SYR_TREPA	06203 rattus norvegicus
7	30	75.0	318	1 RCN2_RAT	Q8db5 streptococcus pneumoniae	
8	30	75.0	447	1 EX7L_STRMU	Q9m06 arabidopsis thaliana	
9	30	75.0	524	1 C90C_ARATH	Q9x43 lutzomyia longipalpus	
10	30	75.0	572	1 SNTD_LUTTOMIA	P39788 saccharomyces cerevisiae	
11	30	75.0	833	1 MBP1_YEAST	Q62880 rattus norvegicus	
12	29	72.5	253	1 T2D7_RAT	Q8bb7 oceanobacillus	
13	29	72.5	351	1 EGCG_OCEINH	P49866 zea mays	
14	29	72.5	571	1 CRTI_HAIZE	P8093 capsicum annuum	
15	29	72.5	582	1 CRTI_JAPAN	P2854 lycopersicon esculentum	
16	29	72.5	583	1 CTD2_YEAST	P53359 saccharomyces cerevisiae	
17	29	72.5	839	1 YO10_YREPA	P0354 treponema pallens	
18	28	70.0	41	1 YES7_YEAST	P40012 saccharomyces cerevisiae	
19	28	70.0	109	1 ATPF_BUCBP	Q89433 buchnera apicalis	
20	28	70.0	156	1 PAPI_MOUSE	P35220 mus musculus	
21	28	70.0	175	1 MAG2_SCOP0	Q94148 schizosaccharomyces pombe	
22	28	70.0	213	1 RS3A_APLOCA	P71019 bacillus subtilis	
23	28	70.0	264	1 PAED_BACSU	Q99112 staphylococcus aureus	
24	28	70.0	317	1 RUVB_STAAM	Q8cb91 staphylococcus aureus	
25	28	70.0	334	1 RUVB_STAAM	Q83457 porcine adrenomedullin	
26	28	70.0	448	1 F1BP_ADEBP3	Q93451 staphylococcus aureus	
27	28	70.0	448	1 TRME_STAAM	Q99133 staphylococcus aureus	
28	28	70.0	459	1 TRME_STAAM	Q8cm05 staphylococcus aureus	
29	28	70.0	459	1 TRME_STAAM	Q9zhd9 buchnera apicalis	
30	28	70.0	473	1 6PGD_BUCBP	P41477 autographa californica	
31	28	70.0	506	1 G7A_NPYAC	Q91463 arthropodopsis thaliana	
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Coulier R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,	Borrelli I., Cummings N.J., Bolotin A., Borchart S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,	Braun M., Brignell S.C., Bron S.,
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
"The nucleotide sequence of Saccharomyces cerevisiae chromosome	Choi S.K., Codani J.J., Connerton I.F., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
XIII.";	Denizot F., Devine K.M., Entian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
Nature 387:90-93 (1997).	Ghislain P., Ghislain P., Golightly E.J., Grandi G.,
-1- SIMILARITY: STRONG, TO YEAST ROTENONE-INSENSITIVE NADH-UBIQUINONE	Guiseppi G., Guy B.J., Haga K., Hailech J., Harwood C.R., Henaut A.,
OXIDOREDUCTASE (ND1).	Hilbert H., Hollsappel S., Hosono S., Hull M.F., Itaya M., Jones L.,
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modified and this statement is not removed. Usage by and for commercial	Medina N., Meliando R.P., Mizuno M., Nakai S., Noback M.,
entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Noone D., O'Reilly M., Ogawa K., Ogihara A., Onodera B., Park S.H.,
EMBL; ZA7071; CAAT7359.1; -.	Parro V., Pohl T.M., Portebele D., Porwollik S., Prescott A.M.,
PIR; S55401; GermOnline; 142815; -.	Prescanec B., Pujic P., Purcell B., Rapoport G., Rey M., Reynolds S.,
SGD; SGD0005753; YMR145C.	Rieger M., Rivoltella C., Rocha E., Roche B., Rose M., Sadale Y.,
GO; GO:0005731; Mitochondrion; IDA.	Sato T., Scanlan E., Schleicher S., Schroeter R., Scoffone F., Soldo B.,
GO; GO:003954; P NADH dehydrogenase activity; IDA.	Sekiuchi J., Sekowska A., Seror S.J., Sevor P., Shin B.S., Soldo B.,
GO; GO:0019655; P ethanol fermentation; IMP.	Sorokin A., Tacconi E., Takahashi H., Takekawa K.,
GO; GO:0006116; P NADH oxidation; IDA.	Takahashi H., Tanaka T., Terpstra P., Tognoni A.,
InterPro; IPR001327; FAD_Pyr_redox.	Takemoto K., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,
InterPro; IPR001327; FAD_Pyr_redox.	Tosato V., Uchiyama S., Vanderholz M., Vannier F., Weitzengger T.,
PFam; PF00070; pyr_redox; 1.	Vianello R., Wedler H., Weidler H., Weitzengger T.,
Ubiquinone.	Viari A., Wambutt R., Weller E., Weller H., Yoshikawa H., Danchin A.,
Ubiquinone.	Yoshida K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Yata K.,
SEQUENCE 560 AA; 62774 MW; 10B1795E12B29C34 CRC64;	Zumstein E., Yoshikawa H.P., Zumstein E., Yoshikawa H., Yata K.,
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Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;	RT subtilis";
CC -1- SIMILARITY: Belongs to the BMP lipoprotein family.	RT subtilis";
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DR InterPro; IPR003760; Bmp.	DR InterPro; IPR003760; Bmp.
DR IntePro; IPR004327; Prok_lipoprot_S.	DR IntePro; IPR004327; Prok_lipoprot_S.
DR pfam; PF005608; Bmp; 1.	DR pfam; PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.
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Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;	Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
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Db 347 RLKTMVKKV 355	Db 269 LSSMVKKK 276

InterPro: IPR008909; tRNA-synt_1d_C.
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 Pfam: PF00750; tRNA-synt_1d; 1.
 Pfam: PF05746; tRNA-synt_1d_C; 1.
 Pfam: PF01329; TRNAINHARG.
 TIGRFAMS; TIGR00456; args; 1.
 PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 Complete proteome.
 SITE 132 142 "HIGH" REGION
 SEQUENCE 589 AA; 67131 MW; FAF156F69P4556BE3 CRC64;
 SQ 1 RLSSMVKY 9

Query Match Score 32; DB 1; Length 589;
 Best Local Similarity 66.67%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 EX7L STRMU STANDARD; PRT; 447 AA.
 ID EX7L STRMU STANDARD; PRT;
 AC Q8DV55;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
 DE (Exonuclease VII large subunit).
 QY 1 RLSSMVKY 9
 Db 66 RLQSIKKI 74

Query Match Score 32; DB 1; Length 589;
 Best Local Similarity 66.67%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 RCN2 RAT STANDARD; PRT; 318 AA.
 ID RCN2 RAT STANDARD; PRT;
 AC Q62703; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulocalbin 2 precursor (Calcium-binding Protein ERC-55) (Taipoxin-associated calcium-binding protein-49) (TCBP-49).
 RN RCN2 OR BRC55.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI TaxID=10116; [1]
 RN "SEQUENCE FROM N.A.
 STRAIN=Sprague-Dawley;
 MEDLINE=9239201; PubMed=7722520;
 RT Dods D, Schlimgen A.K., Lu S.Y., Perin M.S.;
 "Novel reticular calcium binding protein is purified on taipoxin columns."
 J. Neurochem. 64:2339-2344 (1995).
 CC -- FUNCTION: Not known. Binds calcium.
 CC -- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -- TISSUE SPECIFICITY: Ubiquitous.
 CC -- SIMILARITY: Belongs to the CREC family.
 CC -- SIMILARITY: Contains 6 EF hand calcium-binding domains.

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EMBL: AE014902; AAN5819 1; -
 DR HAMAP; MF_00378; -; 1.
 DR InterPro; IPR000774; Aldkhan-dh_hamm.
 DR InterPro; IPR003153; Exonuc_VII_L.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR00365; tRNA_antI.
 Pfam: PF02601; Exonuc_VII_L; 1.
 Pfam: PF01336; tRNA_antI; 1.
 Pfam: PF01336; tRNA_antI; 1.
 Pfam: PF000137; xSEB; 1.
 KW Hydrolase; Nuclease; Exonuclease; Complete Proteome.
 SQ SEQUENCE 447 AA; 51146 MW; 560112CE/DAFAA3 CRC64;

Query Match Score 30; DB 1; Length 447;
 Best Local Similarity 66.7%; Pred. No. 54;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

FT SIGNAL 1 RETICULOCALBIN 2.
 FT SIGNAL 23 RETICULOCALBIN 2.
 CHAIN 24 318 RETICULOCALBIN 2.
 CA_BIND 75 86 EF-HAND 1 (POTENTIAL).
 FT SIGNAL 111 122 EF-HAND 2 (POTENTIAL).
 CA_BIND 163 174 EF-HAND 3 (POSSIBLY ANCESTRAL).
 FT SIGNAL 131 318 MW; 575054FC09FFF CRC64;

RESULT 9

Q90C_ARATH STANDARD; PRT; 524 AA.

ID C90C_ARATH ID: 023242; Last annotation update: 16-OCT-2001 (Rel. 40, Created) 16-OCT-2003 (Rel. 42, Last annotation update)

DT Cytochrome P450 90C1 (BC_1.14.-.-) (ROTUNDIFOLIATA)

OS Arabidopsis thaliana (Mouse-ear cress). "The ROTUNDIFOLIA gene of Arabidopsis thaliana encodes a new member of the cytochrome P-450 family that is required for the regulated polar elongation of leaf cells." [1]

GN R3T3 OR CYP90C1 OR ARA4636380 OR F2A10_980 OR AP22_10 OR F2B13_220.

OC Eukaryota; Viridiplantae; Streptophytai; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophytes; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis; NCBI TaxID=3702; RN [1]

RP SEQUENCE FROM N.A. PubMed=96361880; Kim G.-T., Tsukaya H.-I. Uchimiywa H.; "The ROTUNDIFOLIA gene of Arabidopsis thaliana encodes a new member of the cytochrome P-450 family that is required for the regulated polar elongation of leaf cells." [2]

RN SEQUENCE FROM N.A. STRAIN=Cv, COLUMBIA; MEDLINE=200834688; PubMed=10617198; Mayer K.F.X., Schneller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Tarryn N., Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kraiss M., Deisenay M., Puigdomenech P., Watson M., Banncroft I., Reichert B., Portelette D., Perez-Alonso M., Boultry M., Schmidlindl T., Vos P., Hoheisel J., Zimmerman W., Wedder H., Ridley P., Langham S., Schuewer J., McCullagh B., Bisham L., Robben J., Van der Schueren J., Gromponez B., Chuang Y.-J., Vandenbussche F., Braet M., Weltjens I., Velt M., Bastiaans I., Aert R., Defoor E., Holter B., Brandt A., Peters S., van Staeren M., Hilbert H., Braun M., Meerjman P., Klein Lankhorst R., Rose M., Hauf J., Dirks W., Berneiser S., Hemel S., Feldpausch M., Lambertz S., Koetter P., De Keyser A., Buysshaert C., Giesien J., Villarrel R., De Clercq R., Van Montagu M., Rogers J., Cronin J., Lennard N., McLeay K., Clark L., Doggett J., Hall S., Kay M., Quail M.A., Bray Allen S., RA Petetti A., Rajandream M.A., Lyne M., Benes V., Reichmann S., RA Borrova D., Bloecher H., Schafre M., Grimm M., Lohmert T.-H., RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Grandérath K., Dauner D., Herzel A., RA Neumann S., Argiriou A., Vitali D., Lignori R., Piravandi R., RA Massenet O., Quigley P., Clabaugh G., Muendlein A., Felber R., RA Schnabl R., Hiller R., Schmidt W., Lechtnay R., Aubourg S., RA Cherdor F., Cooke R., Berger C., Monfort A., Casacuberta E., RA Gibbons T., Weber N., Vandenbol M., Barquez M., Tezol J., Torres A., RA Perez-Perez A., Purnelle B., Bent J., Johnson S., Tacon D., Jesse T., RA Heijnen L., Schwart S., Scholler P., Heber S., Francis P., Bielle C., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Rabermann K., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang B., Spiegel L., RA Sekhon M., Murray J., Sheet P., Cordess M., Abu-Threiden J., RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., RA Latreille P., Courtney L., Cloud J., Babbott A., Scott K., Johnson D., RA Minx P., Bentley D., Fulton B., Miller N., Graco T., Kemp K., RA Kramer J., Kramer D., Mards E., Dante M., Pepin K., Billiger L.W., RA Nelson J., Spiech J., Ryan E., Andrews S., Geisel C., Layman D., RA Du H., Ali J., Beghoff A., Jones K., Drono M., Cotton M., Joshi C., RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., RA Ma P., Zhong J., Preston R., Vil D., Sheher M., Matero A., Shah R., RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Hill S., RA Granat S., Shondy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,

RN RLSIMVKV 9
DB 130 RLSQFVKV 138

RA Chen E., Marra M.A., Martienssen R., McCombie W.R.; "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana." [1]

RT Nature 402:769-777(1999).

CC -1- FUNCTION: Might be involved in the biosynthesis of steroids important for the polar elongation of cells during development.

CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (Potential).

CC -1- TISSUE SPECIFICITY: Ubiquitous.

CC -1- CAUTION: Ref. 2 (CAA8139) sequence differs from that shown due to erroneous gene model prediction.

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CC DR AB008097; BAA37167.1; -

EMBL AL161589; CAB0304.1; ALT INIT.

DR 299708; CRB1650.1; ALT INIT.

EMBL AL022141; CAA18139.1; ALT SEQ.

DR IPR001128; Cytochrome_P450.

PRFAM PF00067; P450.1.

PRINTS PR00385; P450.

DR PROSITE PS00087; CYTOCHROME_P450_1.

KW Oxido-reductase; Monoxygenase; Transmembrane; Heme;

KW Endoplasmic reticulum; Multigene family.

FT POTENTIAL_4 24

FT TRANSMEM 4 IRON (HEM) AXIAL LIGAND (BY SIMILARITY).

FT METAL 463 463

FT CONFLICT 45 45 F -> L (IN REF. 2).

SQ SEQUENCE 524 AA; 59389 MW; 5505789308BDDFF272 CRC64;

Query Match Best Local Similarity 75.0%; Score 30; DB 1; Length 524;

Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 1 RLSSMYKVKV 9

Db 266 RLKIQMYKVK 274

RESULT 10

SNP0_LUTLO STANDARD; PRT; 572 AA.

ID SNP0_LUTLO ID: 00000000000000000000000000000000; Q9XZ43;

AC DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

RA Gabel C. 28-FEB-2003 (Rel. 41, Last annotation update)

DE S'-nucleotidase Precursor (EC 3.1.3.5).

GN SNuC.

OS Lukzonita longipalpis (Sand fly).

RA Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Neoptera; Endopterygota; Diptera; Nematoptera; Psychodidae; OC Psychodidae; Lukzonita.

NCBI_TAXID=12000; OX

RN (1) Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.

RC STRAIN=Jacobina; TISSUE=Salivary Gland;

RC Charlab R., Valenzuela J.G., Rowon E.D., Ribeiro J.M.C.; RA "Toward an understanding of the biochemical and pharmacological complexity of the saliva of a hematophagous sand fly, *Lutzomyia longipalpis*."

RT RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RA RN (2) CHARACTERIZATION.

RC TISSUE=Salivary Gland;

RC Ribeiro J.M.C., Rowon E.D., PubMed=10727894;

RX RX MEDLINE=20193550; Ribeiro J.M.C., Rowon E.D., Charlab R.; RA "The salivary 5'-nucleotidase/phosphodiesterase of the hematophagous

RT

IN	sand fly corrected, <i>Lutzomyia longipalpis</i> .";
[3]	Insect Biochem. Mol. Biol. 30:279-285(2000).
ERTRUM	Ribeiro J.M.C., Rowton E.D., Charlton R.; Insect Biochem. Mol. Biol. 30:689-699(2000).
RP	-!- FUNCTION: Degradation of external UDP-glucose to uridine monophosphate and glucose-1-phosphate, which can then be used by the cell (By similarity).
KL	-!- CATALYTIC ACTIVITY: UDP sugar + H(2)O = UMP + sugar 1-phosphate.
CC	-!- CATALYTIC ACTIVITY: A 5'-ribonucleotide + H(2)O = a ribonucleoside + phosphate.
CC	-!- COFACTOR: Zinc (By similarity).
CC	-!- SIMILARITY: Belongs to the 5'-nucleotidase family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; Af132510; ADD32190_1; -.
CC	HSPP; P07024; 2USH; DRR
CC	InterPro; IPR008334; 5'-Nucleotidase_C; InterPro; IPR006146; 5'-Nucleotidase_N; InterPro; IPR006179; 5 nucleotidase; InterPro; IPR004843; N-peptidase; InterPro; IPR004843; N-peptidase; pfam; PF02872; 5_nucleotidaseC; 1; pfam; PF00149; Metallophosph; 1; pfam; PF01607; APYRASE_FAMILY; PROSITE; PS00785; 5_NUCLEOTIDASE_1; 1; PROSITE; PS00786; 5_NUCLEOTIDASE_-1; 1; PROSITE; PS00786; 5_NUCLEOTIDASE_-1; 1; Hydrolase; Glycoprote; Signal; Zinc; SIGNAL; 1 25 POTENTIAL.
CC	PTM
CC	CHAIN 26 572 5' -NUCLEOTIDASE.
CC	CABBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	CABBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	CABBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	SEQUENCE 572 AA; 633531 MW; 69A652338C045316D CRC64 ;
CC	Query Match 75.0%; Score 30; DB 1; Length 572;
CC	Best Local Similarity 75.0%; Pred. No. 67; Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0; Gaps 0;
CC	1 RLSSWTKK 8 : : 70 RVSTWTKK 77
RESULT 11	
MBP1_YEAST	
ID MBP1_YEAST	STANDARD;
AC P39675;	PRT; 833 AA.
DT 01-FEB-1995 (Rel. 31, Created)	
DT 01-FEB-1995 (Rel. 31, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DE Transcription Factor MBP1 (MBF subunit P120).	
DN MBP1 OR YDL056W	
GN Saccharomyces cerevisiae (Baker's yeast).	
OC Eukaryotes; Fungi; Ascomycota; Saccharomycetaceae; Saccharomyces;	
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.	
OX NCBI_TAXID:4932;	
RN [1] _SEQUENCE FROM N.A., AND SEQUENCE OF 372-387.	
RC STRAIN=N1107;	
RX MBDLIN=93313264; PubMed=8372355;	
RA Koch C.; Moll T.; Neuberg M.; Ahorn H.; Nasmyth K.; RT A role for the transcription factors MbP1 and Swi4 in progression from G1 to S phase.; RT Science 261:1551-1557(1993).	

FT	TURN	43	44		DR	InterPro; IPR003162; TFIID-31.
FT	HELIX	47	57		DR	Pfam; PF0291; TFIID-31; 1.
FT	TURN	58	60		DR	ProDom; P001103; TFIID-31; 1.
FT	STRAND	64	66		KW	Transcription regulation; Nuclear protein.
FT	TURN	72	73		FT	DOMAIN 238 251 POLY-ASP
FT	STRAND	75	78		FT	238 AA; 27620 MW; 4045091A9B04378 CRC64;
FT	HELIX	80	89		SQ	253 AA;
FT	TURN	90	91			Query Match 72.5%; Score 29; DB 1; Length 253;
FT	HELIX	93	101			Best Local Similarity 75.0%; Pred. No. 53;
FT	SEQUENCE	833 AA;	93907 MW;			Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
SQ						
QY	1 RLSSMVKK 8					
Db	767 KLSLVRK 774					
RESULT 12						
T2D7 RAT						
ID T2D7 RAT						
AC Q62880;						
DT 01-NOV-1997 (Rel. 35, Created)						
DT 01-NOV-1997 (Rel. 35, Last sequence update)						
DT 15-MAR-2004 (Rel. 43, Last annotation update)						
DT 15-MAR-2004 (Rel. 43, Last annotation update)						
DE Transcription Factor TFIID subunit '(TFIID-31)						
DE (TFIID-32) (TAFII32) (Neuronal cell death related gene in neuron -7)						
DE (DN-7).						
DE TAF9 OR TAF2G OR TAFII31.						
GN Rattus norvegicus (Rat)						
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
NCBI_TaxID=10116;						
OX						
RN						
SEQUENCE FROM N.A.						
RX MEDLINE=9712553; PubMed=9168994;						
RA Nakano T., Shibahara K., Nishimura H., Kikuchi H., Honjo T.; Aoki T., Koike T., Nakano T., Shibahara K., Nishimura H., Kikuchi H., Honjo T.						
RA						
RA						
RT Rat TFIID11 gene is induced upon programmed cell death in differentiated PC12 cells deprived of NGF.						
RL Biochem. Biophys. Res. Commun. 234:230-234 (1997).						
CC						
-!- FUNCTION: TAFs are components of the transcription factor IID (TFIID) complex that are essential for mediating regulation of RNA polymerase transcription. TAFII31 is a coactivator for the P53 protein. Also interacts with the acidic transactivator viral protein 16 (VP16) as well as with the general transcription factor TFIIB (By similarity).						
CC						
CC SUBUNIT: TFIID is composed of TATA binding protein (TBP) and a number of TBP-associated factors (TAFs). TAFII31 and TBP3 bind to each other via amino acid residues in the amino-terminal domain of TBP3 that are essential for transcription. Component of the PCAF complex, at least composed of TAD21/ADA2, TAD31/ADA3, SUP3H, TAF5L/TAF6Sbeta, TAF6/TAF11, TAF6L/PAP65alpha, TAF10/TAF11, TAF10/TAF11, TAF12/TAF12O, TAF9/TAF11 and TRAP. Component of the STAGA transcription coactivator-HAT complex, at least composed of SF3B3/SAP130, GCN5L2, STAF5 gamma/XIFAA0764, TAF5L, TAF6L, TAD31L, TAF10, TAF12, TAF10 and TAF9 (By similarity).						
CC						
CC -!- SIMILARITY: Belongs to the TAF2G family.						
CC						
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CC						
CC DR EMBL; AP004594; BAC12300.1; -.						
CC DR HAMAP; MF_0.820; -; 1.						
CC DR InterPro; IPR00481; DUF258.						
CC DR Pfam; PF03193; DUF258; 1.						
CC DR TIGRFAMS; TIGR00157; TIGR00157; 1.						
CC DR PROSITE; PS50936; ENGC_GTPASE; 1.						
CC KW Hydrolase; GTP-binding; Complete proteome.						
CC DR DOMAIN 109 256 ENGC_GTPASE.						
CC FT NP_BIND 148 151 GTP (PROBABLE).						
CC FT NP_BIND 200 207 GTP (PROBABLE).						
CC FT SITE 255 255 GTP (PROBABLE).						
CC FT SITE 282 295 KNuckle-like cysteine cluster.						
CC SQ SEQUENCE 351 AA; 40008 MW; E0DABBEDEDDB57FP7 CRC54;						
QY 1 RLSSMVKK 9						
Db 89 RFSSIVRKV 97						

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OM protein - protein search, using SW model

Run on: March 1, 2004, 17:20:41 ; Search time 30.3333 Seconds

(without alignments)
93.615 Million cell updates/sec

Title: US-09-905-083-32

Perfect score: 40

Sequence: 1 RLISSMVKKV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_25:*
- 1: sp_bacteria:*
- 2: sp_bacteriophage:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_rhbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	40	100.0	181	4	QBNFV7	Q8nv7 homo sapien
2	40	100.0	253	4	QBN5N9	Q8nv9 homo sapien
3	33	82.5	282	16	O9S208	Q8nv7 anopheles gambiae
4	33	82.5	417	5	QBWTE7	Q8nv8 streptomyces
5	32	80.0	169	16	Q899C6	Q8nv9C6 Clostridium
6	32	80.0	351	17	Q97Z26	Q97Z26 sulfobilous
7	32	80.0	664	3	Q9BP7W7	Q9P7W7 schizosaccharomyces pombe
8	31	77.5	97	9	Q9B021	Q9B021 bacteriophaga
9	31	77.5	390	10	Q8LEQ6	Q8LEQ6 arabidopsis thaliana
10	31	77.5	550	9	Q9W607	Q9W607 bacteriophage
11	31	77.5	589	10	Q7XX91	Q7XX91 oryza sativa
12	31	77.5	610	16	Q8YH8	Q8YH8 leptospira
13	31	77.5	751	10	Q7XMN7	Q7XMN7 oryza sativa
14	31	77.5	912	10	Q9LDK6	Q9LDK6 arabidopsis thaliana
15	31	77.5	2159	10	Q8RVL1	Q8RVL1 zea mays (mexicanus)
16	31	77.5	2159	10	Q8RUQ1	Q8RUQ1 zea mays (mexicanus)

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQUENCE FROM N.A.
TISSUE-Ovarian carcinoma, "Human", Kaushal A., Clements J.A.; RT
RT "Human Keilikrein 7 (KLK7)" short variant mRNA from ovarian carcinoma.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC -1 SIMILARITY: BELONGS TO PEPTIDE FAMILY S1.
DR EMBL: AF411215; AAC03663_1; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR00254; Peptidase_S1A.
DR InterPro; IPR00303; Cys_Ser_trypsin.
DR SMART; SM00020; TRYPSIN DOMAIN.
DR PROSITE; PS50240; TRYPSIN_DOMAIN.
DR PROSITE; PS50135; TRYPSIN_SER; 1.
KW Hydrolyse: Protease; Serine protease.
SQ SEQUENCE 181 AA; 19887 MW; 862AA03BB0C2D78 CRC64;

Title:	US-09-905-083-32	17	30	75.0	105	Q93W83 arabidopsis
Perfect score:	40	18	30	75.0	124	Q8BD39 mus musculus
Sequence:	1 RLISSMVKKV 9	19	30	75.0	131	Q851X1 oryza sativa
Scoring table:	BLOSUM62	20	30	75.0	136	Q8B845 arabidopsis
Gapop 10.0 , Gapext 0.5	21	30	75.0	240	Q17203 caenorhabditis elegans	
1017041 seqs, 315518202 residues	22	30	75.0	308	Q86HA4	
Total number of hits satisfying chosen parameters:	1017041	23	30	75.0	320	Q8BF92
Minimum DB seq length: 0	24	30	75.0	321	Q70341	
Maximum DB seq length: 200000000	25	30	75.0	348	Q8RNK1	
Post-processing: Minimum Match 0%	26	30	75.0	373	Q9V014	
Maximum Match 100%	27	30	75.0	391	Q8CEU9	
Listing first 45 summaries	28	30	75.0	394	Q9CB57	
	29	30	75.0	517	Q94C74	
	30	30	75.0	533	Q8GRH1	
	31	30	75.0	578	Q86PF2 drosophila melanogaster	
	32	30	75.0	647	Q49468 mycoplasma genitalium	
	33	30	75.0	661	Q73B2 xenopus laevis	
	34	30	75.0	690	Q7DQ71 rhodobacter sphaeroides	
	35	30	75.0	815	Q9HEE3 neurospora crassa	
	36	30	75.0	986	Q9UB1 quigelia solani	
	37	30	75.0	1167	Q8PAQ6 xylella fastidiosa	
	38	30	75.0	1167	Q9NAK7 trypanosoma brucei	
	39	30	75.0	1768	Q9GZG6 caenorhabditis elegans	
	40	30	75.0	1887	Q7VA27 prochlorococcus marinus	
	41	29	72.5	99	Q7VZ27	
	42	29	72.5	118	Q40388 nicotiana benthamiana	
	43	29	72.5	119	Q8BXH8 macaca fasciata	
	44	29	72.5	136	Q8XCH6 nicotiana benthamiana	
	45	29	72.5	208	Q8L418 oryza sativa	

ALIGNMENTS

RESULT 1	ID	Q8NFV7	PRELIMINARY;	PRT;	181 AA.
	AC	Q8NFV7;	AC	Q8NFV7;	D
	DT	Q8NFV7;	DT	Q8NFV7;	DT
	DT	Q8NFV7;	DT	Q8NFV7;	DT
	DE	Q8NFV7	DE	Kallikrein 7	DE
	OS	Homo sapiens (Human)	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomi; Mammalia; Eutheria; Primates; Hominidae; Homo.	OS
	OC		OC		OC
	OX	NCBI_TaxID-9606;	OX		OX
	RP	[1]	RP	SEQUENCE FROM N.A.	RP
	RC	TISSUE-Ovarian carcinoma,	RC		RC
	RA	Dong Y., Kaushal A., Clements J.A., RT	RA	"Human Keilikrein 7 (KLK7)" short variant mRNA from ovarian carcinoma.", RA	RA
	RL		RL		RL
	CC	-1 SIMILARITY: BELONGS TO PEPTIDE FAMILY S1.	CC		CC
	DR	EMBL: AF411215; AAC03663_1; -	DR		DR
	DR	GO; GO:0004263; F:chymotrypsin activity; IEA.	DR		DR
	DR	GO; GO:0004233; F:peptidase activity; IEA.	DR		DR
	DR	GO; GO:0004295; F:trypsin activity; IEA.	DR		DR
	DR	GO; GO:0004250; P:proteolysis and peptidolysis; IEA.	DR		DR
	DR	InterPro; IPR001314; Peptidase_S1A.	DR		DR
	DR	InterPro; IPR00254; Peptidase_S1A.	DR		DR
	DR	InterPro; IPR00303; Cys_Ser_trypsin.	DR		DR
	DR	SMART; SM00020; TRYPSIN DOMAIN.	DR		DR
	DR	PROSITE; PS50240; TRYPSIN_DOMAIN.	DR		DR
	DR	PROSITE; PS50135; TRYPSIN_SER; 1.	DR		DR
	KW	Hydrolyse: Protease; Serine protease.	KW		KW
	SQ	SEQUENCE 181 AA; 19887 MW; 862AA03BB0C2D78 CRC64;	SQ		SQ

Qy	1 RLSNMVKV 9	RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wieszorek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)"
Db	51 RLSNMVKV 59	RL Nature 41:141-147 (2002).
		DR EMBL; AL931111; CAB51262.1;
		DR PIR; T35294; T35294; PROK_LIPOPROT_S;
		DR PROTEIN; PS0003.3; FROKAR_LIPOPROTEIN_1.
		KW Complete proteome.
		SEQUENCE 282 AA; 30789 MW; BEECFEE1743703A33 CRC64;
		Query Match 82.5%; Score 33; DB 16; Length 282;
		Best Local Similarity 87.5%; Pred. No. 47;
		Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RLSNMVKK 8	QY 1 RLSNMVKK 8
		DB 265 RLSNMVK 272
		RESULT 4
		QWTE7 PRELIMINARY; PRT; 417 AA.
		ID Q8WTE7
		AC Q8WTE7;
		DT 01-MAR-2002 (TREMBLrel. 20, Created)
		DR GO:0009263; F:chymotrypsin activity; IEA.
		DR GO:0008233; F:peptidase activity; IEA.
		DR GO:0004295; F:trypsin activity; IEA.
		DR GO:000508; P:proteolysis and peptidolysis; IEA.
		DR InterPro:IPR00903; Cys Ser trypsin.
		DR InterPro:IPR01254; Peptidase_S1.
		DR InterPro:IPR01314; Peptidase_S1A.
		PFam:PF00089; trypsin; 1.
		DR SMART:SM00020; T2TF_SPC_1.
		DR PROSITE:PS00240; TRYPSIN_DOMAIN; 1.
		DR PROSITE:PS00134; TRYPSIN_HIS; 1.
		DR PROSITE:PS00115; TRYPSIN_SER; 1.
		KW Hydrolase; Protease; Serine_protease.
		SEQUENCE 253 AA; 27608 MW; 2D686AA1B22A668 CRC64;
		Query Match 100.0%; Score 40; DB 4; Length 253;
		Best Local Similarity 100.0%; Pred. No. 1.2;
		Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RLSNMVKV 9	QY 1 RLSNMVKV 9
		DB 123 RLSNMVKV 131
		SEQUENCE FROM N.A.
		RP Strausberg R./Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
		CC !-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
		DR EMBL; BC03205; AAH32005.1; .
		DR GO: GO:0009263; F:chymotrypsin activity; IEA.
		DR GO: GO:0008233; F:peptidase activity; IEA.
		DR GO:0004295; F:trypsin activity; IEA.
		DR GO:000508; P:proteolysis and peptidolysis; IEA.
		DR InterPro:IPR00903; Cys Ser trypsin.
		DR InterPro:IPR01254; Peptidase_S1.
		DR InterPro:IPR01314; Peptidase_S1A.
		DR PFam:PF00089; trypsin; 1.
		DR SMART:SM00020; T2TF_SPC_1.
		DR PROSITE:PS00240; TRYPSIN_DOMAIN; 1.
		DR PROSITE:PS00134; TRYPSIN_HIS; 1.
		DR PROSITE:PS00115; TRYPSIN_SER; 1.
		KW Hydrolase; Protease; Serine_protease.
		SEQUENCE 253 AA; 27608 MW; 2D686AA1B22A668 CRC64;
		Query Match 100.0%; Score 40; DB 4; Length 253;
		Best Local Similarity 100.0%; Pred. No. 1.2;
		Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RLSNMVKV 9	QY 1 RLSNMVKV 9
		DB 219 RLSNMVKV 227
		RESULT 5
		Q899C6 PRELIMINARY; PRT; 169 AA.
		ID Q899C6
		AC Q899C6;
		DT 01-JUN-2003 (TREMBLrel. 24, Created)
		DR GO:0005549; F:odorant binding; IEA.
		DR GO:0004872; F:olfactory receptor activity; IEA.
		DR GO:0004872; F:receptor activity; IEA.
		DR GO:0007608; P:olfaction; IEA.
		DR InterPro:IPR00117; 7tm_6.
		KW Receptor.
		SEQUENCE 417 AA; 48520 MW; F60D7D7BD93D37F2 CRC64;
		Query Match 82.5%; Score 33; DB 5; Length 417;
		Best Local Similarity 77.8%; Pred. No. 68;
		Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1 RLSNMVKV 9	QY 1 RLSNMVKV 9
		DB 219 RLSNMVKV 227
		SEQUENCE FROM N.A.
		RP STRAIN-A3(2)/M145.
		RX MEDLINE=21936410; PubMed=12000953;
		RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsey T., Howarth S., Huang C.-H., Kissner T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbowitsch E., Rajandream M.A., Rutherford K., Rutledge S., RA
		OC Streptomyces coelicolor.
		OC Streptomyces; Actinobacteria; Actinomycetales.
		OC Streptomyces; Streptomyctaceae; Streptomyces.
		OC NCBI_TAXID=1902;
		RP SEQUENCE-A3(2)/M145.
		RX MEDLINE=21936410; PubMed=12000953;
		RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsey T., Howarth S., Huang C.-H., Kissner T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbowitsch E., Rajandream M.A., Rutherford K., Rutledge S., RA

OX	NCBI_TaxID=1513;							
RN	[1] _SEQUENCE FROM N.A.							
RP	SEQUENCE FROM N.A. / E8B;							
RC	STRAIN=Massachusetts / E8B;							
RX	MEDLINE=2247253; PubMed=12552129;							
RA	Briegmann H., Baumer S., Fricke W.F., Wiezer A., Liesegang H., Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne P., Gottschalk G.;							
RA	"The genome sequence of Clostridium tetani, the causative agent of tetanus disease.", Proc. Natl. Acad. Sci. U.S.A. 100:13116-1321 (2003).							
RT	RT							
RL	AC E015936; AAO3403.1; -.							
DR	GO; GO:0005489; P:Electron transporter activity; IEA.							
DR	GO; GO:005516; P:Iron ion binding; IEA.							
DR	GO; GO:0016431; P:Oxidoreductase activity; IEA.							
DR	GO; GO:0006118; P:Electron transport; IEA.							
DR	GO; GO:006800; P:Oxygen and reactive oxygen species metabolism; IEA.							
DR	InterPro; IPR00345; CytC heme BS.							
DR	InterPro; IPR001989; Radical_G.							
DR	InterPro; IPR007197; Radical_SAM.							
DR	PROSITE; PS001190; CYTOCHROME C; 1.							
DR	PROSITE; PS01087; RADICAL_ACTIVATING_1.							
KW	Oxidoreductase; Complete_proteome.							
SQ	SEQUENCE 169 AA; 19292 MW; CC7AB251D3844C1 CRC64;							
Query Match	Best Local Similarity 75.0%; Pred. No. 49; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;							
Qy	1 RLSSMVKV 8							
Db	85 RLASMIKK 92							
RESULT 6								
Q97226	PRELIMINARY;	PRT;	351 AA.					
ID	Q97226;							
AC								
DT	01-OCT-2001 (TREMBLrel. 18, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)							
DE	Biotin synthase (bioB) (EC 2.8.1.6).							
GN	BIOB OR SS0115.							
OS	Sulfolobus solfataricus.							
OC	Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;							
NCBI_TaxID	2287;							
OX								
RP	SEQUENCE FROM N.A.							
RC	STRAIN=ATCC 35092 / DSM 1617 / P2;							
RX	MEDLINE=1122396; PubMed=11422726;							
RA	She Q., Singh R.K., Conflanokeri P., Zivanovic Y., Allard G., Awayze M.J., Chan-Heiner C.C.-Y., Clausen T.G., Curtis B.A., De Noors A., Brause G., Fletcher D., Gordon P.M.K., Goord C., Heikamp-de Jong I., Jeffries A.C., Kozaera C.J., Medina N., Peng X., Thi Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doellittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sersen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.", Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).							
RL	EMBL; AE006729; AAC41371.1; -.							
DR	PIR; D90264; D90264.							
DR	GO; GO:0004076; P:biotin synthase activity; IEA.							
DR	GO; GO:0016740; P:transerase activity; IEA.							
DR	InterPro; IPR006638; E1b3.							
DR	InterPro; IPR007197; Radical_SAM.							
PFam	PF01055; Radical_SAM; 1.							
KW	SMART; SM00729; E1b3; 1.							
SEQUENCE	Complete_proteome.							
SQ	351 AA; 3984 MW; 892DB90BC987F752 CRC64;							
Query Match	80.0%; Score 32; DB 17; Length 351;							

Query Match	Best Local Similarity 66.7%; Pred. No. 97; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;							
Qy	1 RLSSMVKV 9							
Db	341 RLDSLVIKK 349							
RESULT 7								
Q9PFW7	PRELIMINARY;	PRT;	664 AA.					
ID	Q9PFW7;							
AC	Q9PFW7;							
DT	01-OCT-2000 (TREMBLrel. 15, Created)							
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
DB	Hypothetical Armadillo_beta-catenin domain protein.							
SP	SPBC1703.03C.							
GN	Schizosaccharomyces pombe (Fission yeast).							
OS	Eukaryota; Fungi; Ascomycota; Schizosaccharomyces; Schizosaccharomycetales; Schizosaccharomyces.							
CC	Schizosaccharomyces.							
OC	NCBI_TaxID=4836;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=972h-;							
RA	Rajandream M.A., Barrall B.G., Cadieu E., Lelaure V., Galibert F.,							
RA	Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.							
RL	EMBL; AL36536; CAB66447.1; -.							
DR	EMBL; T50316; T50316.							
DR	GenoDB; SPombe; SPBC1703.03C; -.							
DR	InterPro; IPR00225; Armadillo.							
DR	PFam; PF00514; Armadillo seg; 1.							
DR	PROSITE; PS50176; ARM_REPEAT; 1.							
SQ	SEQUENCE 664 AA; 7481 MW; 363FEB00EB15E69F CRC64;							
Query Match	Score 32; DB 3; Length 664;							
Qy	1 RLSSMVKV 9							
Db	624 RLSSMVKV 632							
RESULT 8								
Q9B021	PRELIMINARY;	PRT;	97 AA.					
ID	Q9B021;							
AC	Q9B021;							
DT	01-JUN-2001 (TREMBLrel. 17, Created)							
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)							
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)							
DB	Hypothetical protein (Fragment).							
OS	Bacteriophage GMSE-1.							
OX	NCBI_TaxID=148339;							
RN	SEQUENCE FROM N.A.							
RA	Cole C., Young S.A., Maudlin I., Welburn S.C.; "Endogenous bacteriophage may influence susceptibility to trypansome infection in tsetse," Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.							
RA	NCBI_TaxID 1.							
RA	NON_TIR							
SQ	SEQUENCE 97 AA; 10987 MW; B170B63BB43F2C52 CRC64;							
Query Match	Score 31; DB 9; Length 97;							
Qy	2 LSMSMVKV 9							

Db	88	IQSMYTKV 95		Best Local Similarity 77.8%; Pred. No. 2.5e+02; Mismatches 1; Indels 0; Gaps 0;
RESULT 9				
QBLE06		PRELIMINARY;	PRT;	390 AA.
ID QBLE06 ; AC QBLE06 ; DT 01-OCT-2002 (TREMBLrel. 22, Created)				
OS Arabidopsis thaliana (Mouse-ear cress). Hypothetical protein.				
DS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; euodiots; core euodiots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OC NCBI_TaxID=3702;				
RN [1]				
SEQUENCE FROM N.A.				
RA Haas B.J., Volkovs N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White C., Salberg S.L.; RT "Full-length messenger RNA sequences greatly improve genome annotation.",				
RT Genome Biol. 0:0-0(2002).				
RN [2]				
SEQUENCE FROM N.A.				
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.; RT "Full-length cDNA from Arabidopsis thaliana", Submitted (MAR-2002) to the ENBL/GenBank/DBJ databases.				
RL Submitted (MAR-2002) to the ENBL/GenBank/DBJ databases.				
DR AY28293; AM22525; 1. -				
DR InterPro: IPR001810; F-box.				
DR InterPro: IPR006652; Keich_rept.				
PFam: PF00646; F-box; 1.				
SMART: SM00256; FBOX; 1.				
RW HYPOTHETICAL PROTEIN.				
SQ SEQUENCE 390 AA; 44992 MW; 2ABA01DDF4E19F72 CRC64;				
Query Match 77.5%; Score 31; DB 10; Length 390; Best Local Similarity 55.6%; Pred. No. 1.8e+02; Mismatches 5; Conservative 3; Indels 0; Gaps 0;				
Db	230	RFSSMIRKI 238		
RESULT 10				
QBW607		PRELIMINARY;	PRT;	550 AA.
ID QBW607 ; AC QBW607 ; DT 01-MAR-2002 (TREMBLrel. 20, Created)				
OS Molecular analysis of Listeria monocytogenes ScottA bacteriophage PSA reveals ribosomal frameshifting as a general mechanism for generation of major structural proteins.".				
DS Submitted (JUN-2001) to the ENBL/GenBank/DBJ databases.				
DR A3312240; CAIC8558.1; -				
DR InterPro: IPR005021; Phage termin.				
PFAM: PF003354; Phage terminase; 1.				
SO SEQUENCE 550 AA; 63915 MW; OF43142D3906F00F CRC64;				
Query Match 77.5%; Score 31; DB 9; Length 550;				

RA Bevan M., Monfort A., Casabuberta E., Puigdomenech P., Hoheisel J.,
 RA Mewes H.W., Lencik K., Mayer K.F.X.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL161595; CAB80638; 1;
 DR EMBL; AL02605; CAB77062; 1;
 DR PIR; HB5470; HB5470;
 DR PIR; T05012; T05012;
 DR InterPro; IPR01810; F-box;
 DR InterPro; IPR00652; Kelch_reP;
 DR PF00646; F-box; 3;
 DR Pfam; PF01344; Kelch; 2;
 DR SMART; SM00256; FBX; 2;
 DR SMART; SM00612; Kelch; 2;
 DR PROSITE; PS50101; FBX; 1;
 DR KW Hypothetical protein;
 DR SEQUENCE 912 AA; 105278 MW; 8C764AFDD114D57E CRC64;
 DR Query Match 77.5%; Score 31; DB 10; Length 912;
 DR Best Local Similarity 55.6%; Pred. No. 4e+02;
 DR Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 DR Qy 1 RLSMMVKV 9
 DR Db 403 RFSSMMRKI 411
 DR RN
 DR SEQUENCE FROM N.A.
 DR Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
 DR Liu Y.L., Mu J., Wu Z., Chen L., Fan D.L., Wang Q.J., Zhang L.,
 DR Liu Y.Q., Yu S.L., Liu X.H., Liu T.R., Zhang Y.J., Lu Y., Li C., Li T.,
 DR Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
 DR Hao P., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
 DR Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
 DR Zhang Y., Cai Z., Chen J., Wang H., Chen X.Y., Shao C.Y., Sun Y.,
 DR Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
 DR Gu J.L., Chen S.T., Ni L., Zhu P.H., Hong G.F.,
 DR Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL606693; CF04521; 1;
 DR SEQUENCE 751 AA; 87386 MW; 7F47A6A44A7182C CRC64;
 DR SQ
 DR SEQUENCE FROM N.A.
 DR Best Local Similarity 77.5%; Score 31; DB 10; Length 751;
 DR Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DR Qy 2 LSSMMVKV 9
 DR Db 404 LSSVVVKV 411
 DR Query Match 77.5%; Score 31; DB 10; Length 751;
 DR Best Local Similarity 87.5%; Pred. No. 3.3e+02;
 DR Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DR RN
 DR SEQUENCE FROM N.A.
 DR Q9LDK6 PRELIMINARY;
 DR ID Q9LDK6;
 DR AC Q9LDK6;
 DR DT 01-OCT-2000 (TREMBIrel. 15, Created)
 DR DT 01-OCT-2000 (TREMBIrel. 15, Last sequence update)
 DR DT 01-OCT-2003 (TREMBIrel. 25, Last annotation update)
 DR DE Hypocalpain protein.
 DR AT4G39750. Arabidopsis thaliana (Mouse-ear cress).
 DR Spermatophytida; Magnoliophytida; Streptophytida; Embryophytida;
 DR Eudicots; Rosids; Brassicales; Brassicaceae; Arabidopsis.
 DR NCBI TaxID:3702;
 DR RN
 DR SEQUENCE FROM N.A.
 DR Monfort A., Casabuberta E., Puigdomenech P., Mewes H.W., Lemcke K.,
 DR Mayer K.F.X.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR [2]
 DR SEQUENCE FROM N.A.
 DR EU Arabidopsis sequencing project;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR RN
 DR SEQUENCE FROM N.A.
 DR [3]
 DR SEQUENCE FROM N.A.

Db :|||:|||
515 RISSMLKE 522

Search completed: March 1, 2004, 17:34:42
Job time : 33.3333 secs

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OM protein - protein search, using SW model

Run on: March 1, 2004, 17:21:46 ; Search time 11.8889 Seconds
 (without alignments), 39.081 Million cell updates/sec

Title: US-09-905-083-33

Perfect score: 40

Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51623971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/.ptodata/2/iaa/5A_COMB.pep:
 2: /cgn2_6/.ptodata/2/iaa/5B_COMB.pep:
 3: /cgn2_6/.ptodata/2/iaa/6A_COMB.pep:
 4: /cgn2_6/.ptodata/2/iaa/6B_COMB.pep:
 5: /cgn2_6/.ptodata/2/iaa/PC1US_COMB.pep:
 6: /cgn2_6/.ptodata/2/iaa/backfiles1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	9	US-09-502-000-33	Sequence 33, Appl
2	40	100.0	9	US-09-518-243-33	Sequence 33, Appl
3	40	100.0	253	US-08-557-146-2	Sequence 2, Appl
4	40	100.0	253	US-08-824-874-3	Sequence 3, Appl
5	40	100.0	253	US-09-154-144-2	Sequence 2, Appl
6	40	100.0	253	US-08-310-188-2	Sequence 2, Appl
7	40	100.0	253	US-09-210-084-3	Sequence 3, Appl
8	40	100.0	253	US-09-764-762-3	Sequence 3, Appl
9	40	100.0	253	FCT-US96-0294-2	Sequence 2, Appl
10	38	95.0	812	US-09-189-039A-12075	Sequence 12075, A
11	36	90.0	9	US-09-502-000-35	Sequence 35, Appl
12	36	90.0	9	US-09-502-000-36	Sequence 36, Appl
13	36	90.0	9	US-09-18-243-35	Sequence 35, Appl
14	36	90.0	9	US-09-918-143-36	Sequence 36, Appl
15	33	82.5	190	US-08-339-152A-19	Sequence 19, Appl
16	33	82.5	190	US-08-007-99B-6	Sequence 6, Appl
17	33	82.5	190	US-08-689-776A-6	Sequence 24312, A
18	33	82.5	447	US-09-252-991A-44312	Sequence 17, Appl
19	33	82.5	634	US-08-319-152A-17	Sequence 16, Appl
20	33	82.5	653	US-08-339-112A-16	Sequence 3, Appl
21	33	82.5	653	US-08-007-99B-3	Sequence 3, Appl
22	33	82.5	653	US-08-689-276A-3	Sequence 24, Appl
23	32	80.0	21	US-08-153-007A-24	Sequence 24, Appl
24	32	80.0	21	US-08-398-196-24	Sequence 22, Appl
25	32	80.0	22	US-08-977-778-22	Sequence 22, Appl
26	32	80.0	235	US-07-940-655A-12	Sequence 12, Appl
27	32	80.0	235	US-08-690-096-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
 US-09-502-000-33
 ; Sequence 33, Application US/09502600A
 ; Patent No. 6794344
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
 ; FILE REFERENCE: D6223CIP-C
 ; CURRENT FILING DATE: 2000-02-11
 ; CURRENT APPLICATION NUMBER: US/09-502, 600A
 ; PRIORITY APPLICATION NUMBER: US/09/039, 211
 ; PRIORITY FILING DATE: 03-14-1998
 ; NUMBER OF SEQ ID NOS: 136
 ; SEQ ID NO 33
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Residues 5-13 of the SCCE protein

RESULT 2
 US-09-502-000-33
 ; Sequence 33, Application US/09918243
 ; Patent No. 667403
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; APPLICANT: Cannon, Martin J.
 ; APPLICANT: Santini, Alessandro
 ; APPLICANT: Santini, Alessandro
 ; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 ; FILE REFERENCE: D6223CIP/C/D/CIP
 ; CURRENT APPLICATION NUMBER: US/09/918, 243
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIORITY APPLICATION NUMBER: US
 ; PRIORITY FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 136
 ; SEQ ID NO 33
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

```

FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0;

Qy      1 LILPLQLL 9
        ||||| | |
Db       1 LILPLQLL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5,834,90
GENERAL INFORMATION:
; APPLICANT: Biegelund, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.5; Mismatches 0; Indels 0;
Mismatches 9; Conservative 0;

Qy      1 LILPLQLL 9
        ||||| | |
Db       5 LILPLQLL 13

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5982300
GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Hillman, Presti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5

```

CORESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0252 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

SEQUENCE INFORMATION:
SEQUENCE FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504

TS-08-824-874-3

Query Match Score: 40; D
Best Local Similarity 100.0%; Pred. No. 2.
Matches 9; Conservative 0; Mismatches 0

1 ILLPLQILL 9
| | | | | | | |
5 ILLPLQILL 13

RESULT 5
US/09/154-344-2
Sequence 2, Application US/09154344
GENERAL INFORMATION:
Patent No. 5981256
APPLICANT: Egelrud, Torbjorn
Hansson, Lennart
Recombinant Stratum C Enzyme (SCCE)
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 110C3326-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEX/FAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLGY: linear
 MOLECULE TYPE: protein

US-09-154-344-2

Query Match Score 40; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2,5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 LLLPQQILL 9
 Db 5 LLLPQQILL 13

RESULT 7
 US-09-210-084-3

Sequence 3, Application US/09210084
 Patent No. 6197511
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/210,084
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/824,874
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0252 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 532504

US-09-210-084-3

Query Match Score 40; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2,5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 LLLPQLL 9
 Db 5 LLLPQLL 13

RESULT 8
 US-09-764-762-3

Sequence 3, Application US/09764762
 Patent No. 647195
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 5

US-08-930-188-2

Query Match Score 40; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2,5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 LLLPQLL 9
 Db 5 LLLPQLL 13

RESULT 6
 US-08-930-188-2

Sequence 2, Application US/08930188
 Patent No. 6093397
 GENERAL INFORMATION:
 APPLICANT: Dixon, Eric P.
 APPLICANT: Johnstone, Edward M.
 APPLICANT: Little, Sheila P.
 TITLE OF INVENTION: APOLOID PRECURSOR PROTEIN PROTEASE AND RELATED NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESS: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: United States of America
 ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/930,188
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/416,257
 FILING DATE: 04-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Blalock, Donna K.
 REGISTRATION NUMBER: 38,082
 REFERENCE/DOCKET NUMBER: X9239
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-277-1090
 TELEFAX: 317-276-3861
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-930-188-2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/764,762
 FILING DATE: 16-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/210,084
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Billing, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0252 US
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 532504
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-764-762.3

Query Match 100.0%; Score 40; DB 4; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 LILPQLILL 9
 Db 5 LILPQLILL 13

RESULT 9
 PCT-US96-042244-2
 Sequence 2, Application PC/TUS9604294
 GENERAL INFORMATION:
 APPLICANT: Dixon, Eric P.
 APPLICANT: Johnston, Edward M.
 APPLICANT: Little, Sheila P.
 TITLE OF INVENTION: AYLOID PRECURSOR PROTEIN PROTEASE AND
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 ZIP: 46285
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/04294
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/416,257
 FILING DATE: 04-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Blalock, Donna K.
 REGISTRATION NUMBER: 38,082
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-277-1090
 TELEX/FAX: 317-276-3861
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-0294-2

RESULT 10
 US-09-489-039A-12075
 Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LILPQLILL 9
 Db 5 LILPQLILL 13

RESULT 11
 US-09-489-039A-12075
 Sequence 12075, Application US/09489039A
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 FILE REFERENCE: 2709_2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO: 12075
 LENGTH: 812
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12075

RESULT 11
 US-09-502-600-35
 Sequence 35, Application US/09502600A
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 TITLE OF INVENTION: Ovarian Cancer
 FILE REFERENCE: D6223CIP-C
 CURRENT FILING DATE: 2000-02-11
 CURRENT APPLICATION NUMBER: US/09/502,600A
 PRIOR APPLICATION NUMBER: 09/039,211
 PRIOR FILING DATE: 03-14-1998
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 35
 LENGTH: 9

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Residues 6-14 of the SCCE protein

US - 09 - 502 - 600 - 35

Query Match 90.0%; Score 36; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 2 LIPQLQIL 9
 Db 1 LIPQLQIL 8

RESULT 12
 US - 09 - 502 - 600 - 36
 Sequence 36; Application US/09502600A
 Patent No. 629344
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
 FILE REFERENCE: D6223CIP-C
 CURRENT FILING DATE: 2000-02-11
 CURRENT APPLICATION NUMBER: US/09/502,600A
 PRIOR APPLICATION NUMBER: 09/039,211
 PRIOR FILING DATE: 03-14-1998
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO 36
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Residues 4-12 of the SCCE protein

US - 09 - 502 - 600 - 36

Query Match 90.0%; Score 36; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 LIPQLQIL 8
 Db 2 LIPQLQIL 9

RESULT 14
 US - 09 - 918 - 243 - 36
 Sequence 36; Application US/09918243
 Patent No. 6627403
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Cannon, Martin J.
 APPLICANT: Santin, Alessandro
 TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D6223CIP/C/DCIP
 CURRENT APPLICATION NUMBER: US/09/918,243
 CURRENT FILING DATE: 2001-07-30
 PRIORITY NUMBER: US - 09 - 502 - 600 - 35
 PRIOR APPLICATION NUMBER: 2000-07-13
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO 36
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Residues 4-12 of the SCCE protein

US - 09 - 918 - 243 - 36

Query Match 90.0%; Score 36; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 LIPQLQIL 8
 Db 2 LIPQLQIL 9

RESULT 15
 US - 08 - 339 - 152A - 19
 Sequence 19; Application US/08339152A
 Patent No. 5643726
 GENERAL INFORMATION:
 APPLICANT: Tanzi, Rudolph E.
 APPLICANT: Kovacs, Dora M.
 TITLE OF INVENTION: Methods For Modulating Transcription (APP) Promoter
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 New York Ave., NW, Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/339,152A
 FILING DATE: 10-NOV-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 0609.4120000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 TELEX:

RESULT 13
 US - 09 - 918 - 243 - 35
 Sequence 35; Application US/09918243
 Patent No. 6627403
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Cannon, Martin J.
 APPLICANT: Santin, Alessandro
 TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D6223CIP/C/D/CP
 CURRENT FILING DATE: 2001-07-30
 PRIORITY NUMBER: US - 09 - 918 - 243 - 35
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO 35
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 6-14 of the SCCE protein

US - 09 - 918 - 243 - 35

Query Match 90.0%; Score 36; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

; INFORMATION FOR SEQ ID NO: 19;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-19

Query Match 82.5%; Score 33; DB 1; Length 190;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	LILPLQILL	9
		:	
Db	1	LILPLSILL	9

Search completed: March 1, 2004, 17:38:23
Job time : 11.8889 secs

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILPQLIL 9
 DB 1 LILPQLIL 9

RESULT 2
 ABG23378 standard; protein; 136 AA.
 XX AC ABG23378;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #23369.
 XX KW Human; chromosome mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSEB-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DRP; 2001-639362/73.
 XX N-ISDB; AAS87565.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20: SEQ ID NO 53737; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG10377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent do not appear in the printed specification, but was obtained in electronic form directly from WIPO at ftw.wipo.int/Pub/published_pct_sequences

Sequence 136 AA;

Query Match 100.0%; Score 40; DB 4; Length 136;
 CC Best Local Similarity 100.0%; Pred. No. 9.3;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILPQLIL 9
 DB 11 LILPQLIL 19

RESULT 3
 ADA05736 standard; protein; 198 AA.
 XX AC ADA05736;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human NOV18C protein SEQ ID NO:96.
 XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective;
 XX KW anti-parkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haemopoietic disorder; dyslipidaemia.
 XX OS Homo sapiens.
 XX PN WO2003029424-A2.
 XX PD 10-APR-2003.
 XX PR 02-OCT-2002; 2002WMO-US031373.
 XX PR 02-OCT-2001; 2001US-0326483P.
 XX PR 05-OCT-2001; 2001US-0327443P.
 XX PR 05-OCT-2001; 2001US-0327449P.
 XX PR 09-OCT-2001; 2001US-0327917P.
 XX PR 09-OCT-2001; 2001US-0328029P.
 XX PR 09-OCT-2001; 2001US-0328044P.
 XX PR 09-OCT-2001; 2001US-0328056P.
 XX PR 12-OCT-2001; 2001US-0328492P.
 XX PR 15-OCT-2001; 2001US-0328414P.
 XX PR 17-OCT-2001; 2001US-0330142P.
 XX PR 18-OCT-2001; 2001US-0330399P.
 XX PR 22-OCT-2001; 2001US-0341058P.
 XX PR 24-OCT-2001; 2001US-0332266P.
 XX PR 29-OCT-2001; 2001US-0341957P.
 XX PR 17-APR-2002; 2002US-0373817P.
 XX PR 19-APR-2002; 2002US-0373818P.
 XX PR 19-APR-2002; 2002US-0373817P.
 XX PR 19-APR-2002; 2002US-0373826P.
 XX PR 22-APR-2002; 2002US-0373844P.
 XX PR 16-MAY-2002; 2002US-0374977P.
 XX PR 16-MAY-2002; 2002US-0381037P.
 XX PR 16-MAY-2002; 2002US-0381042P.
 XX PR 17-MAY-2002; 2002US-0315622P.
 XX PR 29-MAY-2002; 2002US-0381656P.
 XX PR 25-JUN-2002; 2002US-033831P.
 XX PR 01-OCT-2002; 2002US-0391335P.
 XX (CURA-) CURAGEN CORP.

PI Smithson G, Milliet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; PI Patterajan M, Spyrek KA, Edinger SR, Ellerman K, Malaykar UK; PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; PI Ji W, Miller C, Rastelli L, Stone DJ, Perna CR, Shency SG; PI Shimets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Spaderna SK; PI Eisen AJ, Ganguli EA, Rieger DK, Dipippo VA; DR WPI; 2003-381226/36. N-PSDB; ADA05735.

XX New NOVX polypeptides and nucleic acids useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidaemia, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; Page 170; 586pp; English.

PS The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have anti-diabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and anti-lipidemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disease, immune disorders such as Alzheimer's disease or Parkinson's neurodegenerative disorders such as Alzheimers disease or various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

XX Sequence 198 AA;

Query Match 100.0%; Score 40; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 13; O; Indels 0; Gaps 0;

QY 1 LILPLQLL 9
Db 5 LILPLQLL 13

RESULT 4
ADA05732
ID ADA05732 standard; protein; 250 AA.
XX AC ADA05732;
DT 06-NOV-2003 (first entry)
XX Human Nov18a protein SEQ ID NO:92.

KW human; NOVX; antiislaetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX Homo sapiens.

PN WO2003029424-A2.
XX 10-APR-2003.
PD
XX PF -OCT-2002; 2003WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327415P.
PR 09-OCT-2001; 2001US-0327443P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328844P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330144P.
PR 18-OCT-2001; 2001US-0330303P.
PR 22-OCT-2001; 2001US-0341055P.
PR 24-OCT-2001; 2001US-0339265P.
PR 29-OCT-2001; 2001US-0343622P.
PR 01-NOV-2001; 2001US-0349575P.
PR 17-APR-2002; 2002US-0373267P.
PR 19-APR-2002; 2002US-0373811P.
PR 19-APR-2002; 2002US-0373822P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381044P.
PR 17-MAY-2002; 2002US-0381045P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383833P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.

XX PA (CUBA) CURAGEN CORP.

XX XX Smithson G, Miller I, Peyman JA, Kakuda R, Ju J, Li L, Guo X; Patrakian M, Syprett KA, Edinger SR, Ellerman K, Malyankar JM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shney SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolfi EA, Rieger DK, Spaderna SK;

XX DR N-PDB; ADA05731.

XX WPI: 2003-381626/36.
XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidaemia, and in chromosome mapping, tissue typing or pharmacogenomics.

XX CC Claim 1; Page 169-170; 586pp; English.
XX DR N-PDB; ADA05731.

XX CC The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell binds to the polypeptide described above; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interaction of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to

OS

CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipasemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

XX Sequence 250 AA;
 SQ Query Match 100.0%; Score 40; DB 6; Length 250;
 XX Best Local Similarity 100.0%; Pred. No. 17;
 AC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PR Qy 1 LLLPQILL 9
 XX Db 2 LLLPQILL 10

RESULT 5

AAR67888
 ID AAR67888 standard; protein; 253 AA.
 XX

AC AAR67888;
 XX DT 25-MAR-2003 (revised)
 XX DT 09-AUG-1995 (first entry)
 DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
 XX PW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
 KW callosities; keratosis pilaris; ichthyoses; eczema.
 XX OS Homo sapiens.
 PN W09500651-A1.
 XX PD 05-JAN-1995.
 XX PF 20-JUN-1994; 94NO-IB000166.
 XX PR 18-JUN-1993; 93DK-00000725.
 PA (SYMB-) SYMBICOM AB.

XX PI Egelrud T, Hansson L;
 XX WPI: 1995-052088/07.
 DR N-PSDB; AAQ81203.

XX Disclosure: Page 97; 137pp; English.
 PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
 PT related vectors, transformed cells and polypeptides, useful for treating
 PT skin disorders, e.g. acne or psoriasis, and for identification of
 PT specific inhibitor.

XX PS The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
 CC and skin care products, especially to treat and prevent acne, xerosis,
 CC or other hyperkeratotic conditions (e.g. callosities or keratoses
 CC pilaris) ichthyoses, psoriasis, eczema, etc. It is produced
 CC recombinantly following mammal, insect, plant, or microorganism
 CC transformation with plasmid PS507. (Updated on 25-MAR-2003 to correct EN

CC field.)
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 40; DB 2; Length 253;
 XX Best Local Similarity 100.0%; Pred. No. 17;
 AC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PR Qy 1 LLLPQILL 9
 XX Db 5 LLLPQILL 13

RESULT 6

AAW0383
 ID AAW0383 standard; protein; 253 AA.
 XX AC AAW0383;
 XX DT 31-DEC-1996 (first entry)
 XX DE Human amyloid precursor protein protease.
 KW Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
 KW Therapy.
 XX OS Homo sapiens.
 PN W09631122-A1.
 XX PD 10-OCT-1996.
 XX PR 02-APR-1996; 96WO-US0042294.
 XX PR 04-APR-1995; 95US-00416257.
 XX PA (ELIL) LILLY & CO ELI.
 XX PI Dixon EP, Johnstone EM, Little SP;
 XX DR WPI: 1996-464694/46.
 XX DR N-PSDB; AAT39783.
 XX PT New isolated human amyloid precursor protein protease - used to develop
 PT prods. for the treatment or diagnosis of associated conditions, esp.
 PT Alzheimer's disease.
 XX PS Claim 1; Page 44-45; 55pp; English.
 XX Human amyloid precursor protein protease (AAW0383) is involved in the
 CC processing or clearance of amyloid precursor Protein to form beta-amyloid
 CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
 CC obtcd. from a human lung library. Recombinant protease can be produced in
 CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
 CC (partic. AV-120 host cells. It is used to develop products for the design
 CC and testing of cpds. useful for treating or preventing conditions
 CC associated with beta-amyloid peptide, esp. Alzheimer's disease
 XX Sequence 253 AA;

Query Match 100.0%; Score 40; DB 2; Length 253;
 XX Best Local Similarity 100.0%; Pred. No. 17;
 AC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PR Qy 1 LLLPQILL 9
 XX Db 5 LLLPQILL 13

RESULT 7

ABB84421
 ID ABB84421 standard; peptide; 253 AA.
 XX

AC ABB84421;
 XX DE Human SCCE protein N-terminal fragment SEQ ID 48.
 XX DT 08-NOV-2002 (First entry)
 XX PR 09-FEB-2002; 2002WO-IB001300.
 XX PR 09-FEB-2001; 2001CA-02332655.
 XX PR 09-FEB-2001; 2001DK-000000218.
 XX PA (EGEL/.) EGELRUD T.
 XX PA (HANS/.) HANSSON L.
 XX WPI; 2002-643380/69.
 XX PT Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
 XX PS Example 6; Page 37; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous SCCE or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an inflammatory skin disease selected from diseases consisting of epidermal hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal fragment of the human stratum corneum chymotryptic enzyme, SCCE fragment with human kallikrein 7 (KUK7), used in the development of the transgenic mammals described in the invention.

XX Sequence 253 AA:
 Query Match Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sq 1 LILPLQIL 9
 Db 5 LILPLQIL 13

Query Match Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sq 1 LILPLQIL 9
 Db 5 LILPLQIL 13

RESULT 8
 ABB84406

RESULT 9
 AAU82740 standard; protein; 253 AA.
 ID AAU82740
 XX DE Protein differentially regulated in prostate cancer #43.
 AC DT 28-JAN-2003 (first entry)
 XX DE Prostate cancer; Gene expression; differential regulation;
 DE DE molecular marker; drug target; cancer detection; cancer diagnosis;
 DE DE cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX DE Homo sapiens.
 XX DE OS WO20021638-A2.
 XX DE XX WO20021638-A2.
 XX DE PD 17-OCT-2002.
 XX DE OS 08-APR-2002; 2002KC-US010824.
 XX DE PN 06-APR-2001; 2001US-0281731P.
 XX DE PR 06-APR-2001; 2001US-0281732P.
 XX DE PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX DE PI Sun 2, Jay G;
 XX DE PR WPI; 2003-058520/05.
 XX DE DR N-PSDB; ABX10343.
 XX DE PT Novel Genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX DE XX Claim 1; Page 293-294; 416pp; English.
 XX CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, Grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood, etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX SQ Sequence 253 AA;
 XX SQ Query Match 100.0%; Score 40; DB 5; Length 253;
 XX Best Local Similarity 100.0%; Pred. No. 17;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 LILPLQILL 9
 XX Db 5 LILPLQILL 13
 XX SQ RESULT 10
 XX ABU07440

Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 LLLPLQLL 9
 Db 5 LLLPLQLL 13

RESULT 11

ID ABU0471 standard; protein; 253 AA.
 XX AC ABU0471;
 XX DT 28-JAN-2003 (first entry)
 DE Protein differentially regulated in prostate cancer #74.
 XX KW Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX OS Homo sapiens.
 XX PN WO200281638-A2.
 XX PD 17-OCT-2002.
 XX PP 08-APR-2002; 2002WO-US010824.
 XX PR 06-APR-2001; 2001US-0281711P.
 XX PR 06-APR-2001; 2001US-0281732P.
 XX PA (ORIG-) ORIGEN TECHNOLOGIES INC.
 XX PI Sun Z, Jay G;
 XX DR 2003-058520/05.
 XX DR N-PSDB; ABX10375.

PT Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

PT Claim 1; Page 351; 416pp; English.

XX The invention describes genes (I) which are differentially regulated in prostate cancer. (I) is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, staging, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus

CC for searching specific binding partners of the polypeptide (I) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in Pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer

XX Sequence 253 AA;

Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLPLQLL 9
 Db 5 LLLPLQLL 13

RESULT 12

ID ABR58471 standard; protein; 253 AA.
 XX AC ABR58471;
 XX DT 07-JUL-2003 (first entry)
 DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
 XX KW Human; cytosstatic; gene therapy; vaccine; cancer; ovarian cancer.
 XX OS Homo sapiens.
 XX PN WO2003029468-A1.
 XX PD 10-APR-2003.
 XX PR 02-OCT-2002; 2002WO-US031467.
 XX PR 02-OCT-2001; 2001US-03227135P.
 XX PR 30-MAY-2002; 2002US-0384531P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Algate PA, Mannion J;
 XX DR 2003-372001/35.

PT New Polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.

PS Claim 2; Page 157-158; 169pp; English.

CC The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention

SQ Sequence 253 AA;

Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLPLQLL 9
 Db 5 LLLPLQLL 13

RESULT 13

ADB80484
 ID ADB80484 standard; protein; 253 AA.
 XX AC ADB80484;
 XX DT 04-DEC-2003 (first entry)
 DE Ovarian cancer-associated protein #24.
 XX KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
 post-operative chemotherapy; radiation therapy; tumour prognosis;
 pre-cancerous lesion detection.
 XX OS Homo sapiens.
 XX PN WO200102235-A2.
 PD 27-DEC-2002.
 PP 18-JUN-2002; 2002WO-US019297.
 XX PR 18-JUN-2001; 2001US-0299234P.
 PR 27-AUG-2001; 2001US-0315287P.
 PR 05-SEP-2001; 2001US-031754P.
 PR 13-NOV-2001; 2001US-0350646P.
 PR 12-APR-2002; 2002US-0372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PI Mack DH, Gish KC;
 WPI; 2003-167431/16.
 DR N-PSDB; ADB80483.
 XX Detecting an ovarian cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
 PT Claim 13; Page 291; 332PP; English.
 CC The invention relates to a method of detecting an ovarian cancer-associated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 40; DB 7; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLLPLQIIL 9
 Db 5 LLLPLQIIL 13

RESULT 14
 AAB21326
 ID AAB21326 standard; protein; 257 AA.
 XX AC AAB21326;
 XX DT 02-FEB-2001 (first entry)

XX Human HSCEE.
 XX Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; HSCEE;
 XX human stratum corneum chymotrypsin-like enzyme; kallikrein-like protein;
 XX serine protease; cytostatic; cancer; prostate cancer; prostrate cancer.
 OS Homo sapiens.
 XX PN WO200053776-A2.
 PD 14-SEP-2000.
 XX PP 09-MAR-2000; 2000WO-C2000258.
 XX PR 11-MAR-1999; 99US-0124260P.
 PR 01-APR-1999; 99US-0127389P.
 PR 21-JUL-1999; 99US-0144919P.
 XX PA (MOUNT SINAI HOSPITAL.
 PI Yousef GM, Diamandis EP;
 WPI; 2000-587440/55.
 XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.
 PT Example 4; Fig 17; 18pp; English.
 XX Sequence 257 AA;
 CC The present sequence is human stratum corneum chymotryptic enzyme (HSCEE), member of the kallikrein multi-gene family. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used to treat conditions mediated by the kallikrein-like proteins.
 XX Sequence 257 AA;
 CC Query Match 100.0%; Score 40; DB 3; Length 257;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLLPLQIIL 9
 Db 5 LLLPLQIIL 13

RESULT 15
 AAB03240
 ID AAB03240 standard; peptide; 9 AA.
 XX AC AAB03240;
 XX DT 01-NOV-2001 (first entry)
 DE Human stratum corneum chymotrypsin peptide #5 (residues 6-14).
 XX Stratum corneum chymotrypsin enzyme peptide #5 (residues 6-14).
 XX cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
 KW anti-sense therapy; malignant hyperplasia.
 XX OS Homo sapiens.

XX WO200159158-A1.
 XX BN 16-AUG-2001.
 PD XX

PF 07-FEB-2001; 2001WO-US003977.
 XX
 PR 11-FEB-2000; 2000US-00502600.
 XX
 PA (UTAR-) UNIV ARKANSAS.
 XX
 PI O'brien TJ;
 XX
 DR WPI; 2001-514676/56.
 XX
 PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin
 PT enzyme.
 XX
 PS Claim 25, Page 103; 127PP; English.

XX
 WPI; 2001-514676/56.

XX
 Diagnosing cancer comprises detecting stratum corneum chymotrypsin
 PT enzyme.

XX
 Claim 25, Page 103; 127PP; English.

CC The invention relates to diagnosing cancer especially ovarian cancer, by
 CC screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
 CC considered to be an integral part of tumour growth and metastasis, and
 CC therefore, markers indicative of their presence or absence are useful for
 CC the diagnosis of cancer. The method is useful for diagnosing cancer,
 CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
 CC to treat a cancer selected from ovarian, breast, lung, colon, prostate
 CC and other cancers in which SCCE is overexpressed. The present sequence is
 CC human SCCE peptide
 XX
 SQ Sequence 9 AA;

```
Query Match Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Prod. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LLPLQILL 9
      ||||| |
Db 1 LLPLQILL 8
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Search completed: March 1, 2004, 17:28:49
 Job time : 47.5556 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:35:01 ; Search time 24.1111 Seconds

(without alignments)
78.818 Million cell updates/sec

Title: US-09-905-083-33

Perfect score: 40

Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters:

809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	40	100.0	9	US-09-918-243-33	Sequence 33, Appl
2	40	100.0	9	US-09-905-083-33	Sequence 33, Appl
3	40	100.0	253	9 US-09-B888-615-38	Sequence 98, Appl
4	40	100.0	253	9 US-09-764-762-3	Sequence 3, Appl
5	40	100.0	253	14 US-10-264-283-90	Sequence 90, Appl
6	40	100.0	253	15 US-10-295-027-498	Sequence 498, Appl
7	40	100.0	253	15 US-10-173-999-48	Sequence 48, Appl
8	36	90.0	9	US-09-918-243-35	Sequence 35, Appl
9	36	90.0	9	US-09-918-243-36	Sequence 16, Appl
10	36	90.0	253	9 US-09-905-083-35	Sequence 35, Appl
11	36	90.0	9	US-09-905-083-36	Sequence 36, Appl
12	34	85.0	23	US-09-864-761-16097	Sequence 45097, Appl
13	34	85.0	201	10 US-09-956-622A-39	Sequence 39, Appl
14	33	82.5	516	14 US-10-156-761-11235	Sequence 11235, Appl
15	32	80.0	21	13 US-10-096-241-24	Sequence 24, Appl

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NAME: KEY: CHAIN

US-09-918-243-33

; OTHER INFORMATION: Residues 5-13 of the SCCE protein

US-09-918-243-33

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

US-09-918-243-33

; OTHER INFORMATION: Residues 5-13 of the SCCE protein

US-09-918-243-33

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

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US-09-918-243-33

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; ORGANISM: Homo sapiens

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; ORGANISM: Homo sapiens

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US-09-918-243-33

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US-09-918-243-33

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; ORGANISM: Homo sapiens

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US-09-918-243-33

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US-09-918-243-33

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US-09-918-243-33

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US-09-918-243-33

; OTHER INFORMATION: Residues 5-13 of the SCCE protein

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US-09-918-243-33

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US-09-918-243-33

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; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

US-09-918-243-33

Page 2

APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: DE223CIP/C/Div
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
-09-005-083-33

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RESULT 3
S-09-888-615-98
Sequence No. Application US/09888615
Patent No. US20020048561
GENERAL INFORMATION: GREGORY
APPLICANT: PLIMMAN

APPLICANT : GENEPEL, SEAN
APPLICANT : CHARYDZAK, GLEN
APPLICANT : MANNING, GERALD
APPLICANT : SUDARSHAN, SUCHA
TITLE OF INVENTION : NOVEL PROTEASES

FILE REFERENCE: US09/114
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047

NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 98 LENGTH: 253

LIFE: FRI
ORGANISM: *Homo sapiens*

Best Local Similarity 100.0%; Pred. No. 19;
 Matches 9; Conservative 0; Mismatches 0; Indels

MY 1. INTRODUCTION 9

5 LLLLQILL 13

IS-09-764-762-3
Semence 3 Application US/09764762

Patent No. US20020068341A1
GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
Lal, Preeti

NUMBER OF SEQUENCES: 5

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CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 52504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

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US-10-264-283-90
Sequence 90, Application US/10264283
Publication No. US20030144494A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121:590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
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Db      5 LLLPQLILL 13

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RESULT 6
US-10-295-027-498
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Publication No. US2003023350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezsi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and File Reference: 018501-0125001S
CURRENT APPLICATION NUMBER: US/10/295,027
PRIORITY FILING DATE: 2002-11-13
PRIORITY APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/356,666
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/324,393
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 498
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-498

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 LLPLQLL 13

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US-10-173-999-48
Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions and Methods of Screening for Modulators of Ovarian Cancer
FILE REFERENCE: 018501-002420US
CURRENT FILING DATE: 2002-06-17
PRIORITY APPLICATION NUMBER: US/10/173,999
PRIOR FILING DATE: 2001-06-17
NUMBER OF SEQ ID NOS: 136

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 LLPLQLL 13

RESULT 8
US-09-918-243-35
Sequence 35, Application US/09918243
Patent No. US2002014217A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santini, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO: 35
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
US-09-918-243-36
Sequence 36, Application US/09918243
Patent No. US20020142317A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santini, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: US/09/918,243
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO: 36

LENGTH: 9
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 ORGANISM: Homo sapiens
 NAME/KEY: CHAIN
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 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO 36

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RESULT 10
 US-09-905-083-35
 Sequence 35, Application US/09905083
 Patent No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 Ovarian Cancer
 CURRENT APPLICATION NUMBER: D6223CIP/C/Div
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US/09/905,083
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO 35
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
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 SEQ ID NO 35

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 Db 1 LLLPQLL 8

RESULT 11
 US-09-905-083-36
 Sequence 36, Application US/09905083
 Patent No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 Ovarian Cancer
 CURRENT APPLICATION NUMBER: D6223CIP/C/Div
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US/09/905,083
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
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 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
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 US-09-905-083-36

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Db 11 LILPQLLL 18

RESULT 13
 US-09-956-622A-39
 Sequence 39 Application US/0956622A
 Publication No. US20030091973A1
 GENERAL INFORMATION:
 APPLICANT: Horesovsky, Gregory J
 APPLICANT: NO. US20030091973A1 II, L. Staton
 APPLICANT: Rana, Debasish
 TITLE OF INVENTION: Method of Identifying Osteoregenerative Agents Using
 TITLE OF INVENTION: Differential Gene Expression
 FILE REFERENCE: 21402-445
 CURRENT APPLICATION NUMBER: US/09/956,622A
 CURRENT FILING DATE: 2001-09-19
 PRIOR FILING DATE: 2000-09-19
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 39
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 TYPE: PRT
 ORGANISM: Rattus norvegicus

US-09-956-622A-39

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 US-10-156-761-11235
 Sequence 11235 Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIIKU
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
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 LENGTH: 516
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 ORGANISM: Streptomyces avermitilis

US-10-156-761-11235

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Db 8 LILPQLLL 16

Search completed: March 1, 2004, 18:08:50
 Job time : 25.1111 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 1, 2004, 17:21:46 ; Search time 11.8889 Seconds

(without alignments);

39.081 Million Cell updates/sec

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SUMMARIES

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	3 US-09-502-600-31	Sequence 31, Appl
2	49	100.0	9	3 US-09-502-600-89	Sequence 89, Appl
3	49	100.0	9	3 US-09-502-600-109	Sequence 109, Appl
4	49	100.0	9	4 US-09-918-243-31	Sequence 31, Appl
5	49	100.0	9	4 US-09-918-243-89	Sequence 89, Appl
6	49	100.0	9	4 US-09-918-243-109	Sequence 109, Appl
7	49	100.0	144	4 US-09-618-259-4	Sequence 4, Appl
8	49	100.0	154	3 US-09-261-416-7	Sequence 7, Appl
9	49	100.0	224	3 US-09-944-83-33	Sequence 33, Appl
10	49	100.0	225	2 US-08-557-146-12	Sequence 12, Appl
11	49	100.0	225	2 US-09-027-337-4	Sequence 4, Appl
12	49	100.0	225	2 US-09-154-344-12	Sequence 12, Appl
13	49	100.0	225	4 US-09-644-600-4	Sequence 4, Appl
14	49	100.0	225	4 US-09-654-600A-4	Sequence 4, Appl
15	49	100.0	253	2 US-08-557-146-2	Sequence 2, Appl
16	49	100.0	253	2 US-08-824-874-3	Sequence 3, Appl
17	49	100.0	253	2 US-09-154-344-2	Sequence 2, Appl
18	49	100.0	253	3 US-08-930-188-2	Sequence 2, Appl
19	49	100.0	253	3 US-09-210-084-3	Sequence 3, Appl
20	49	100.0	253	4 US-09-764-762-3	Sequence 3, Appl
21	49	100.0	253	5 PCT-US96-04294-2	Sequence 2, Appl
22	39	79.6	9	3 US-09-502-600-12	Sequence 12, Appl
23	39	79.6	9	4 US-09-243-122	Sequence 12, Appl
24	37	75.5	9	3 US-09-502-600-93	Sequence 93, Appl
25	37	75.5	9	4 US-09-918-243-93	Sequence 93, Appl
26	37	75.5	463	4 US-09-540-336-3942	Sequence 2942, Appl
27	33	67.3	204	4 US-09-323-872A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
 US-09-502-600-31
 Sequence 31, Application US/09502600A
 i Patent No. 6294344

i GENERAL INFORMATION:
 i APPLICANT: O'Brien, Timothy J.
 i TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
 i FILE REFERENCE: D6223CIP-C
 i CURRENT FILING DATE: 2000-02-11
 i CURRENT APPLICATION NUMBER: US/09/502,600A
 i PRIOR APPLICATION NUMBER: 09-039,211
 i PRIOR FILING DATE: 03-14-1998
 i NUMBER OF SEQ ID NOS: 136
 i SEQ ID NO: 31
 i LENGTH: 9
 i TYPE: PRT
 i FEATURE:
 i OTHER INFORMATION: Residues 72-80 of the SCCE protein
 i ORGANISM: Homo sapiens
 i US-09-502-600-31

Query Match 100.0%; Score 49; DB 3; Length 9;
 Best Local Similarity 100.0%; Conserv 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTHVL 9
 Db 1 KMNEYTHVL 9

RESULT 2
 US-09-502-600-89
 Sequence 89, Application US/09502600A
 i Patent No. 6294344

i GENERAL INFORMATION:
 i APPLICANT: O'Brien, Timothy J.
 i TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
 i FILE REFERENCE: D6223CIP-C
 i CURRENT FILING DATE: 2000-02-11
 i CURRENT APPLICATION NUMBER: US/09/502,600A
 i PRIOR APPLICATION NUMBER: 09-039,211
 i PRIOR FILING DATE: 03-14-1998
 i NUMBER OF SEQ ID NOS: 136
 i SEQ ID NO: 89
 i LENGTH: 9
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i FEATURE:

OTHER INFORMATION: Residues 72-80 of the SCCE protein
S-09-502-600-89

1 KOMNEYTVHL 9

Query Match 100.0%; Score 49; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels

RESULT 5
US-09-918-243-89
; Sequence 89, Application US/09918243

RESULT 3
-5-09-502-600-109
Sequence 109, Application US/09502600A
Patent No. 6294344
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early
DIAGNOSIS OF CANCER
FILE REFERENCE: D6223CTP-C
CURRENT FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US/09/502,600A
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santini, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D622.CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 89
LENGTH: 9
TYPE: PRT
FEATURE:
ORGANISM: Homo sapiens
NAME/KEY:
OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-89

LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 72-80 of the SCCE protein
S-S-09-502-600-109

Query Match 100.0%; Score 49; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels

RESULT 6 100
DB 1 KMNEIVVHL 9

1 KNEEYTVHL 9
1 KNEEYTVHL 9

Sequence 109, Application US/09918243
Patent No. 6627403
GENERAL INFORMATION:

RESULT 4
S-09-918-243-31
Sequence 31, Application US/09918243
Patent No. 6627403
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Alessandro
APPLICANT: Santini, Martin J.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/DCIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
DRAFTED BY: [REDACTED]
DRAFTED ON: [REDACTED]

APPLICANT: Cannon, Martin J.
APPLICANT: Santini, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6221CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US 09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO: 109
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: *Homo sapiens*
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 72-80 of the SCCE protein

```

i  NAME/KEY: CHAIN
i  OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-109

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Prd. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy  1 KMNNEYVHIL 9

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Query Match 100.0%; Score 49; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels

RESULT 7
Db 1 KMNEYTVHL 9

GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: No. 6642016j Extracellular Serine Protease
 FILE REFERENCE: D6022CIP2
 CURRENT APPLICATION NUMBER: US/09/618,259
 CURRENT FILING DATE: 2000-07-18
 PRIOR APPLICATION NUMBER: US 09/127,444
 PRIOR FILING DATE: 1998-08-21
 NUMBER OF SEQ ID NOS: 72
 SEQ ID NO 4
 LENGTH: 144
 TYPE: PRT
 ORGANISM: unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
 US-09-618-259-4

Query Match 100.0%; Score 49; DB 4; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KNEYTVHL 9
 Db 9 KNEYTVHL 17

RESULT 9
 US-09-261-416-7
 Sequence 7, Application US/09261416A
 Patent No. 6591663
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: TADG-12: A No. 6291663j Transmembrane Serine Protease
 FILE REFERENCE: D6192
 CURRENT APPLICATION NUMBER: US/09/261,416A
 CURRENT FILING DATE: 1999-03-03
 NUMBER OF SEQ ID NOS: 14
 SEQ ID NO 7
 LENGTH: 154
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Chymotryptic enzyme (Scce) homologous to similar
 US-09-261-416-7

Query Match 100.0%; Score 49; DB 3; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVHL 9
 Db 18 KNEYTVHL 26

RESULT 9
 US-08-944-483-33
 Sequence 33, Application US/08944483
 Patent No. 6232456
 GENERAL INFORMATION:
 APPLICANT: COHEN, MAURICE
 APPLICANT: COLPITS, TRACEY L.
 APPLICANT: FRIEDMAN, PAULA N.
 APPLICANT: GRANADOS, EDWARD N.
 APPLICANT: KLAES, MICHAEL R.
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: STEWART, KENT D.

APPLICANT: STROUPE, STEVEN D.
 TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
 AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
 TITLE OF INVENTION: OF THE PROSTATE
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/944,483
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6783.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEFAX: 847/938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 224 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6232456E
 US-08-944-483-33

Query Match 100.0%; Score 49; DB 3; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KNEYTVHL 9
 Db 43 KNEYTVHL 51

RESULT 10
 US-08-557-146-12
 Sequence 12, Application US/08557146
 Patent No. 5834290
 GENERAL INFORMATION:
 APPLICANT: Egelrud, Torbjorn
 APPLICANT: Hansson, Leinart
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case, Patent Department
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113
 MOLECULE TYPE: Polypeptide
 US-08-557-146-12
 SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQ ID NO: 12:

Query Match	100.0%	Score 49;	DB 2;	Length 225;
Best Local Similarity	100.0%	Pred. No. 0.021;		
Matches	9;	Conservative	0;	Gaps 0;
Qy	1 KMNNEYTVHL 9			
Db	44 KMNNEYTVHL 52			

RESULT 11
 US-09-027-337-4
 / Sequence 4, Application US/09027337B
 / Patent No. 5972616
 / GENERAL INFORMATION:
 / APPLICANT: O'Brien, Timothy J.
 / APPLICANT: Tanimoto, Hirotoshi
 / TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
 / TITLE OF INVENTION: Breast and Ovarian Carcinomas
 / FILE REFERENCE: D6054
 / CURRENT APPLICATION NUMBER: US/09/027,337B
 / CURRENT FILING DATE: 1998-02-20
 / NUMBER OF SEQ ID NOS: 13
 / SEQ ID NO 4
 / LENGTH: 225
 / TYPE: PRT
 / ORGANISM: Unknown
 / FEATURE:
 / OTHER INFORMATION: Serine protease catalytic domain of Scc6 homologous to
 / TADG-15
 / US-09-027-337-4
 Query Match

100.0%	Score 49;	DB 2;	Length 225;	
Best Local Similarity	100.0%	Pred. No. 0.021;		
Matches	9;	Conservative	0;	Gaps 0;
Qy	1 KMNNEYTVHL 9			
Db	44 KMNNEYTVHL 52			

RESULT 12
 US-09-154-344-12
 / Sequence 12, Application US/09154344
 / Patent No. 5981256
 / GENERAL INFORMATION:
 / APPLICANT: Egelrud, Torbjorn
 / APPLICANT: Hasson, Lennart
 / TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 / NUMBER OF SEQUENCES: 17
 / ADDRESSEE: White & Case, Patent Department
 / STREET: 1155 Avenue of the Americas
 / CITY: New York

STATE: New York
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/154,344
 FILING DATE: 16-SEP-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: polypeptide
 US-09-154-344-12
 Query Match

100.0%	Score 49;	DB 2;	Length 225;	
Best Local Similarity	100.0%	Pred. No. 0.021;		
Matches	9;	Conservative	0;	Gaps 0;
Qy	1 KMNNEYTVHL 9			
Db	44 KMNNEYTVHL 52			

RESULT 13
 US-09-644-600-4
 / Sequence 4, Application US/09644600
 / Patent No. 6451500
 / GENERAL INFORMATION:
 / APPLICANT: O'Brien, Timothy J.
 / APPLICANT: Tanimoto, Hirotoshi
 / TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
 / FILE REFERENCE: D6064CIP/D
 / CURRENT APPLICATION NUMBER: US/09/644,600
 / CURRENT FILING DATE: 2000-08-23
 / PRIORITY APPLICATION NUMBER: 09/41,213
 / PRIORITY FILING DATE: 1999-10-20
 / PRIORITY APPLICATION NUMBER: 09/027,337
 / PRIORITY FILING DATE: 1998-02-20
 / NUMBER OF SEQ ID NOS: 98
 / SEQ ID NO 4
 / LENGTH: 225
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: SCCE
 / US-09-644-600-4
 Query Match

100.0%	Score 49;	DB 4;	Length 225;	
Best Local Similarity	100.0%	Pred. No. 0.021;		
Matches	9;	Conservative	0;	Gaps 0;
Qy	1 KMNNEYTVHL 9			
Db	44 KMNNEYTVHL 52			

RESULT 14
 US-09-154-344-12
 / Sequence 12, Application US/09154344
 / Patent No. 5981256
 / GENERAL INFORMATION:
 / APPLICANT: Egelrud, Torbjorn
 / APPLICANT: Hasson, Lennart
 / TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 / NUMBER OF SEQUENCES: 17
 / ADDRESSEE: White & Case, Patent Department
 / STREET: 1155 Avenue of the Americas
 / CITY: New York

RESULT 14
 US-09-654-600A-4
 Sequence 4 Application US/09654600A
 i Patent No. 649741
 i GENERAL INFORMATION:
 i APPLICANT: O'Brien, Timothy J.
 i APPLICANT: Tanimoto, Hirotoshi
 i TITLE OF INVENTION: TAG-15: An Extracellular Serine Protease
 i FILE REFERENCE: D604CIP/D
 i CURRENT APPLICATION NUMBER: US/09/654,600A
 i PRIORITY DATE: 2000-09-01
 i PRIOR APPLICATION NUMBER: 09/421,213
 i PRIOR FILING DATE: 1999-10-20
 i NUMBER OF SEQ ID NOS: 98
 i SEQ ID NO 4
 i LENGTH: 225
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i FEATURE:
 i OTHER INFORMATION: SCCE
 US-09-654-600A-4

Query Match 100.0%; Score 49; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNETYTVHL 9
 Db 72 KNNETYTVHL 80

RESULT 15
 US-08-557-146-2
 Sequence 2 Application US/08557146
 i Patent No. 5834290
 i GENERAL INFORMATION:
 i APPLICANT: Egelrud, Torbjorn
 i APPLICANT: Hansson, Lennart
 i TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 i NUMBER OF SEQUENCES: 17
 i CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case, Patent Department
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTY: U.S.A.
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 813-8783
 TELEFAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid

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לעון מודולר וטקטיקת מלחמה

run on: March 1, 2004, 17:16:55 ; Search time 45.5555 Seconds
run on: March 1, 2004, 17:16:55 ; Search time 45.5555 Seconds
protein - protein search, using b/w model

ISSN-0973-0837-31

perfect score: 49
average: 19
standard deviation: 9

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Gap8p 1.0.0 , Gapexec 0.3

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Maximum DB seed length: 2000000000

Cast -processsing: Minimum Match 0%

Maximizing first 45 summaries

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3: geneseqp20018:*

4:

geneseesgt2003as:*

ed. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

Result No.	Score	Query Match	Length	DB ID	Description
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2	49	100.0	9	4 AAE02236	Aae02236 Human STR
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4	49	100.0	136	4 ABG22378	Abg22378 Novel human
5	49	100.0	181	6 ADA05738	Ada05738 Human NOV
6	49	100.0	198	6 ADA05736	Ada05736 Human NOV
7	49	100.0	224	6 ADA05744	Ada05744 Human NOV
8	49	100.0	225	4 AAB98502	Aab98502 Human STR
9	49	100.0	247	6 ADA05742	Ada05742 Human NOV
10	49	100.0	250	6 ADA05732	Ada05732 Human NOV
11	49	100.0	252	6 ADA05734	Ada05734 Human NOV
12	49	100.0	253	2 AAR67988	Aar67988 Human STR
13	49	100.0	253	2 AAW05393	Aaw05393 Human amy
14	49	100.0	253	5 ABB84421	Abb84421 Human SCC
15	49	100.0	253	5 ABB84406	Abb84406 Human SCC
16	49	100.0	253	5 AauB2740	AauB2740 Amino acid
17	49	100.0	253	6 ABU07440	Abu07440 Protein d
18	49	100.0	253	6 ABU07471	Abu07471 Protein d
19	49	100.0	253	6 ABR58471	AbR58471 Human str
20	49	100.0	253	7 ADB80484	Adb80484 Ovarian c
21	49	100.0	257	3 AAB21326	Aab21326 Human HSC
22	49	81.6	226	5 ABB84422	Abb84422 Rat SCCE
23	39	79.6	9	4 AAE08326	Aae08326 Human STR
24	37	75.5	9	4 AAE08295	Aae08295 Human STR
		75.5	9	4 AEE04420	Aee04420 Bovine SCCE
		72.1	9	4 AEE04419	Aee04419 Bovine SCCE

ALIGNMENTS

RESULT 1
 AAE08294 Human stratum corneum chymotrypsin enzyme peptide #59 (residues 72-80).
 ID AAE08294 standard; Peptide; 9 AA.
 XX
 AC AAE08294;
 XX DT 01-NCV-2001 (first entry)
 XX DE Human stratum corneum chymotrypsin enzyme; SCCE; cytosstatic; vaccine; tumour;
 XX KW Stratum corneum chymotrypsin enzyme; SCCE; cytosstatic; vaccine; carcinoma; human;
 KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
 KW antisense therapy; malignant hyperplasia.
 KW

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES						
Result No.	Score	Query Match No.	Length	ID	Description	%
1	4.9	100	0	9	APE08294	99.9
2	4.9	100	0	9	APE08236	Human S
3	4.9	100	0	97	ADA05740	Human M
4	4.9	100	0	136	ABG23378	Novel M
5	4.9	100	0	181	ADA05738	Human M
6	4.9	100	0	198	ADA05736	Human M
7	4.9	100	0	224	ADA05744	Human M
8	4.9	100	0	225	ABK8502	Human S
9	4.9	100	0	247	ADA05742	Human M
10	4.9	100	0	250	ADA05732	Human S
11	4.9	100	0	252	ADA05734	Human M
12	4.9	100	0	253	ABR67888	Human S
13	4.9	100	0	253	AW05383	Human
14	4.9	100	0	253	ABB84421	Human S
15	4.9	100	0	253	ABB84406	Human S
16	4.9	100	0	253	ABU07240	Amino
17	4.9	100	0	253	ABU07440	Protein
18	4.9	100	0	253	ABU07471	Protein
19	4.9	100	0	253	ABR58471	Human
20	4.9	100	0	253	ADB00484	Ovarian
21	4.9	100	0	257	AB21326	Human L
22	4.0	81	6	226	ABG84422	Rat SC
23	3.9	79	6	9	AAE03326	Human
24	3.7	75	5	9	AAE08298	Human
25	3.7	75	5	9	MDP04140	Human

Post-processing : Database :					
Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
A Geneseq 29Jan04: *					
1: geneseqD1980s:*	2: geneseqD1990s:*	3: geneseqD100s:*	4: geneseqD2001s:*	5: geneseqD2002s:*	6: geneseqD2003s:*
7: geneseqD2004s:*	8: geneseqD2004s:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
%					
Result No.	Score	Query Match	Length	DB	ID
1	49	100.0	9	4	ADE08294
2	49	100.0	9	4	ADE08236
3	49	100.0	97	6	ADA05740
4	49	100.0	136	4	ABg23378
5	49	100.0	181	6	ADA05738
6	49	100.0	198	6	ADA05736
7	49	100.0	224	6	ADA05744
8	49	100.0	225	4	ABg85050
9	49	100.0	247	6	ADA05742
10	49	100.0	250	6	ADA05732
11	49	100.0	252	6	ADA05734
12	49	100.0	253	2	Aar67888
13	49	100.0	253	2	Aw005383
14	49	100.0	253	2	ABg84421
15	49	100.0	253	5	ABg84406
16	49	100.0	253	7	ABg84240
17	49	100.0	253	6	ABg07440
18	49	100.0	253	6	ABg07471
19	49	100.0	253	6	ABg8471
20	49	100.0	253	7	ADB010484
21	49	100.0	257	3	AAB21326
22	49	81.6	226	5	ABg84422
23	39	79.6	9	4	AAE03326
24	37	75.5	9	4	AAE08298
25	37	75.5	9	2	ABg84414
26	37	75.5	9	2	ABg84414
27	37	75.5	9	2	ABg84414
28	37	75.5	9	2	ABg84414
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30	37	75.5	9	2	ABg84414
31	37	75.5	9	2	ABg84414
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33	37	75.5	9	2	ABg84414
34	37	75.5	9	2	ABg84414
35	37	75.5	9	2	ABg84414
36	37	75.5	9	2	ABg84414
37	37	75.5	9	2	ABg84414
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62	37	75.5	9	2	ABg84414
63	37	75.5	9	2	ABg84414
64	37	75.5	9	2	ABg84414
65	37	75.5	9	2	ABg84414
66	37	75.5	9	2	ABg84414
67	37	75.5	9	2	ABg84414
68	37	75.5	9	2	ABg84414
69	37	75.5	9	2	ABg84414
70	37	75.5	9	2	ABg84414
71	37	75.5	9	2	ABg84414
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75	37	75.5	9	2	ABg84414
76	37	75.5	9	2	ABg84414
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96	37	75.5	9	2	ABg84414
97	37	75.5	9	2	ABg84414
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101	37	75.5	9	2	ABg84414
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127	37	75.5	9	2	ABg84414
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129	37	75.5	9	2	ABg84414
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146	37	75.5	9	2	ABg84414
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155	37	75.5	9	2	ABg84414
156	37	75.5	9	2	ABg84414
157	37	75.5	9	2	ABg84414
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162	37	75.5	9	2	ABg84414
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165	37	75.5	9	2	ABg84414
166	37	75.5	9	2	ABg84414
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213	37	75.5	9	2	ABg84414
214	37	75.5	9	2	ABg84414
215	37	75.5	9	2	ABg84414
216	37	75.5	9	2	ABg84414
217	37	75.5	9	2	ABg84414
218	37	75.5	9	2	ABg84414
219	37	75.5	9	2	ABg84414
220	37	75.5	9	2	ABg84414
221	37	75.5	9	2	ABg84414
222	37	75.5	9	2	

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0

Matches 9; Conservative 9; Artisense 0; Standard, peptide; 9 AA.

RESULT 2
SEQUENCE08236
AABE08236 Human stratum corneum chymotrypsin enzyme peptide #1 (residues 72-80).
01-NOV-2001 (first entry)
Human stratum corneum chymotrypsin enzyme peptide #1 (residues 72-80).
Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; artisense therapy; malignant hyperplasia.
Homo sapiens.
WO2001159158-A1.
16-AUG-2001.
07-FEB-2001; 2001WO-US003977.
11-FEB-2000; 2000US-00502600.
(UYAR-) UNIV ARKANSAS.
O'brien TJ;
WPI; 2001-514676/56.
Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
Claim 25; Page 102; 127pp; English.
The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is a human SCCE peptide.

Sequence 9 AA;

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0
Matches 9; Conservative 9; Standard, peptide; 9 AA.

RESULT 3
SEQUENCE05740
ADA05740 Human NOV18e protein SEQ ID NO:100.
06-NOV-2003 (first entry)
Human NOV18e protein SEQ ID NO:100.

XX	KW	human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
XX	KW	immunomodulator; cytostatic; neurotropic; neuroprotective;
XX	KW	anti-parkinsonian; anti-lipaemic; gene therapy; human disease;
XX	KW	metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
XX	KW	neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX	KW	immune disorder; haematopoietic disorder; dyslipidaemia.
OS	OS	Homo sapiens.
XX	XX	WO2003029424-A2.
XX	XX	PN
PD	PD	10-APR-2003.
XX	XX	02-OCT-2002; 2002WO-US031373.
XX	XX	02-OCT-2001; 2001US-0326483P.
PR	PR	05-OCT-2001; 2001US-0327435P.
PR	PR	05-OCT-2001; 2001US-0327449P.
PR	PR	09-OCT-2001; 2001US-0322917P.
PR	PR	09-OCT-2001; 2001US-0328029P.
PR	PR	09-OCT-2001; 2001US-0328044P.
PR	PR	09-OCT-2001; 2001US-0328054P.
PR	PR	12-OCT-2001; 2001US-0328056P.
PR	PR	15-OCT-2001; 2001US-0328849P.
PR	PR	17-OCT-2001; 2001US-0330142P.
PR	PR	18-OCT-2001; 2001US-0330309P.
PR	PR	22-OCT-2001; 2001US-0341058P.
PR	PR	24-OCT-2001; 2001US-0339266P.
PR	PR	24-OCT-2001; 2001US-0341629P.
PR	PR	29-OCT-2001; 2001US-0349515P.
PR	PR	01-NOV-2001; 2001US-03443357P.
PR	PR	17-APR-2002; 2002US-0372260P.
PR	PR	19-APR-2002; 2002US-0373815P.
PR	PR	19-APR-2002; 2002US-0373817P.
PR	PR	19-APR-2002; 2002US-0373826P.
PR	PR	20-APR-2002; 2002US-0373884P.
PR	PR	22-APR-2002; 2002US-0374377P.
PR	PR	16-MAY-2002; 2002US-0381037P.
PR	PR	16-MAY-2002; 2002US-0381038P.
PR	PR	16-JAY-2002; 2002US-0381042P.
PR	PR	17-MAY-2002; 2002US-0381642P.
PR	PR	28-MAY-2002; 2002US-0381656P.
PR	PR	29-MAY-2002; 2002US-0381831P.
PR	PR	25-JUN-2002; 2002US-0391335P.
PR	PR	01-OCT-2002; 2002US-000262511.
XX	XX	(CURA-) CURAGEN CORP.
XX	XX	Smithson G., Millet I., Peyman JA., Kekuda R., Ju J., Li L., Guo X., Patturajam M., Spyker KA., Edinger SR., Malayan K., Malyankar UM; Ort T., Gorman L., Zerhouni D.W., Anderson DW., Zheng M., Catterton E.; Ji W., Miller CE., Rastelli L., Stone DJ., Pena CEA., Shenoy SG.; Shimkets RA., Rothenberg ME., Leach MD., Agree ML., Berghs C., Dipippo Eisen AJ., Gangolli EA., Rieder DK., Spaderna SK;, Dipippo C., Gangolli EA., Rieder DK., Spaderna SK;
XX	XX	WPI; 2003-381626/36. N-PSDB; ADA05739.
XX	XX	The Present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) an antibody comprising the above vector; (6) an antibody that immunospecifically
PS	PS	Claim 1; Page 171; 586pp; English.

CC binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of, or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have anti-diabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, anti-parkinsonian and antilipemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

XX

Sequence 97 AA;

Query Match	100.0%	Score 49;	DB 6;	Length 97;
Best Local Similarity	100.0%;	Pred. No. 0.081;		
Matches	9;	Conservative	0;	Mismatches 0;
			Indels 0;	Gaps 0;

Qy 1 KNNETYVHL 9

Db 53 KNNETYVHL 61

RESULT 4
ABG23378 standard; protein; 136 AA.

ID ABG23378;

XX

AC ABG23378;

XX

DE 18-FEB-2002 (first entry)

XX

Human diagnostic protein #23369.

XX

KW Human; chromosome mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

Homo sapiens.

XX

PN WO200175067-A2.

XX

PR 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

XX

PR 23-AUG-2000; 2000US-00649167.

PA (HYSEQ INC.

XX

P1 Drmanac RT, Liu C, Tang YT;

XX

DR WPI: 2001-619362/73.

DR N-PSDB; AASB7565.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

biodiversity.

XX

PS Claim 20; SEQ ID NO 53737; 103PP; English.

XX

The invention relates to isolated polynucleotide (I) and polypeptide (II). Sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and in recombinant production of (III). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, its molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (III). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ

Sequence 136 AA;

Query Match

100.0%; Score 49;

DB 4;

Length 136;

Best Local Similarity

100.0%;

Pred. No. 0.12;

Matches

9;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339265P.
 PR 24-OCT-2001; 2001US-0344629P.
 PR 29-OCT-2001; 2001US-034975P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-037260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-037817P.
 PR 19-APR-2002; 2002US-037826P.
 PR 19-APR-2002; 2002US-037844P.
 PR 22-APR-2002; 2002US-037947P.
 PR 16-MAY-2002; 2002US-038037P.
 PR 16-MAY-2002; 2002US-03810P.
 PR 16-MAY-2002; 2002US-038042P.
 PR 17-MAY-2002; 2002US-038142P.
 PR 28-MAY-2002; 2002US-038164P.
 PR 29-MAY-2002; 2002US-038831P.
 PR 25-JUN-2002; 2002US-039335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX PA (CURA-) CURAGEN CORP.
 XX SQ Sequence 181 AA;
 Query Match 100.0%; Score 49; DB 6; Length 181;
 Best Local Similarity 100.0%; Pred. NO. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KMNEYTVHL 9
 Db 53 KMNEYTVHL 61
 RESULT 6
 ADA05736 standard; protein; 198 AA.
 ID ADA05736
 XX AC ADA05736;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human NOV18c protein SEQ ID NO:96.
 XX KW human; NOX; antidiabetic; anorectic; antibacterial; viricide;
 XX KW immunomodulator; cyostatic; nootropic; neuroprotective;
 XX KW antiparkinsonian; antilipaemic; gene therapy; human disease;
 XX KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 XX KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 XX KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX OS Homo sapiens.
 XX PN WO2003029424-A2.
 XX PD 10-APR-2003.
 XX DF 02-OCT-2002; 2002WO-US031373.
 XX PR 02-OCT-2001; 2001US-0326483P.
 XX PR 05-OCT-2001; 2001US-0324435P.
 XX PR 05-OCT-2001; 2001US-0327449P.
 XX PR 09-OCT-2001; 2001US-0327917P.
 XX PR 09-OCT-2001; 2001US-0328029P.
 XX PR 09-OCT-2001; 2001US-0328044P.
 XX PR 09-OCT-2001; 2001US-032856P.
 XX PR 12-OCT-2001; 2001US-0328549P.
 XX PR 15-OCT-2001; 2001US-0329414P.
 XX PR 17-OCT-2001; 2001US-033014P.
 XX PR 18-OCT-2001; 2001US-0330409P.
 XX PR 22-OCT-2001; 2001US-034058P.
 XX PR 24-OCT-2001; 2001US-033956P.
 XX PR 24-OCT-2001; 2001US-034362P.
 XX PR 01-NOV-2001; 2001US-034975P.
 XX PR 17-APR-2002; 2002US-037477P.
 XX PR 16-MAY-2002; 2002US-037826P.
 XX PR 16-MAY-2002; 2002US-037815P.
 XX PR 19-APR-2002; 2002US-0379317P.
 XX PR 19-APR-2002; 2002US-0379826P.
 XX PR 22-APR-2002; 2002US-037984P.
 XX PR 29-MAY-2002; 2002US-034657P.
 XX PR 16-MAY-2003; 2003US-0381037P.
 XX PR 16-MAY-2003; 2003US-0381038P.
 XX PR 17-MAY-2002; 2002US-0381042P.
 XX PR 28-MAY-2002; 2002US-0381642P.
 XX PR 29-MAY-2004; 2004US-038381P.
 XX PR 25-JUN-2002; 2002US-0391335P.
 XX PR 01-OCT-2002; 2002US-00262511.
 XX (CURA-) CURAGEN CORP.
 XX PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 XX PI Paturajan M, Spytek KA, Boinger SR, Ellerman K, Malvankar UM;
 XX PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX DR N-FSDB; ADA05735.

XX WPI: 2003-381626/36.
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1, Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. Nov1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, anticancer, and antiinflammatory activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

XX Sequence 198 AA;

Query Match 100.0%; Score 49; DB 6; Length 198;
 Best Local Similarity 100.0%; Pred. No. 0.18%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVHL 9
 Db 72 KNEYTVHL 80

RESULT 7
 ADA05744 ID ADA05744 standard; protein; 224 AA.
 XX AC ADA05744;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human NOV18g protein SEQ ID NO:104.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antiparkinsonian; gene therapy; human disease;

XX KW

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haemato poetic disorder; dyslipidaemia.

XX DR Homo sapiens.

XX PN WO2003029424-A2.

XX PD 10-APR-2003.

XX PR 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0325483P.

XX PR 05-OCT-2001; 2001US-0327443P.

XX PR 09-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 12-OCT-2001; 2001US-0328056P.

XX PR 15-OCT-2001; 2001US-0328849P.

XX PR 17-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0331039P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 29-OCT-2001; 2001US-034139P.

XX PR 01-NOV-2001; 2001US-0349575P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373888P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383556P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391338P.

XX PR 01-OCT-2002; 2002US-00262511.

XX PA (CURAGEN CORP.

XX PR Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; PI Patterajan M, Spytek KA, Edinger SR, Elleerman K, Malayankar UM; PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Carterton E; PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergnas C, Dipippo VA; PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; PA

XX DR WPI: 2003-381626736.

XX PR N-PSDB; ADA05743.

XX

CC The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. Nov1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above

CC Claim 1; Page 172; 586pp; English.

CC PR New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

CC

polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytidotab, nootropic, neuroprotective, anti-parkinsonian and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

Homo sapiens.

0200129056-A1.

6-APR-2001.

0-OCT-2000; 2000W0-US029095.

0-OCT-1999; 99US-00421213.

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Over-extracellular serine protein overexpressed in carcinoma

Treatment, prevention of cancer

Example 10; FIG 1; 130PP; Eng.

The present invention relates

ENTER THE WORLD OF

PR 01-OCT-2002; 2002US-00262511.
 XX PA (CUBA-) CURAGEN CORP.
 XX PI Smithson G, Miller I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patterson M, Spyrek KA, Edlinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Miller CE, Zernusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenvoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Gangolli EA, Bergs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX DR N-FSDB; ADA05741.
 XX PR WPI; 2003-381626/36.
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX PS Claim 1; Page 172; 586pp; English.
 XX CC The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. Nov1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipasemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.
 XX SQ Sequence 247 AA;
 Qy Query Match 100.0%; Score 49; DB 6; Length 247;
 CC Best Local Similarity 100.0%; Pred. No. 0.23%; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 9; Conservative 0; DR
 Qy 1 KNEYTVHL 9
 - Db 58 KNEYTVHL 66

RESULT 10
 ADA05732 ID ADA05732 standard; protein: 250 AA.
 XX AC ADA05732;
 XX

DT 06-NOV-2003 (first entry)
 XX Human NOV1a protein SEQ ID NO:92.
 XX PR WO2003029624-A2.
 XX PD 10-APR-2003.
 XX PR 02-OCT-2002; 2002WO-US031373.
 XX PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0330309P.
 PR 24-OCT-2001; 2001US-0330266P.
 PR 24-OCT-2001; 2001US-033629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 19-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373844P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381042P.
 PR 28-MAY-2002; 2002US-033656P.
 PR 29-MAY-2002; 2002US-038383P.
 PR 25-TUN-2002; 2002US-039133P.
 PR 01-OCT-2002; 2002US-00262511.
 XX PA (CUBA-) CURAGEN CORP.
 XX PR Smithson G, Milliet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patterson M, Spytek KA, Edlinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenvoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Gangolli EA, Spaderna SK;
 PR WPI; 2003-381626/36.
 XX DR N-PSDB; ADA05731.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX PR Claim 1; Page 169-170; 586pp; English.
 XX CC The present invention describes NOVX Proteins, where X can be 1 to 55 (e.g. Nov1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid

CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC developmental anomalies. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

XX Sequence 250 AA;

Qy	1	KMNEYTVHL	9
Db	69	KMNEYTVHL	77

XX Query Match Best Local Similarity 100.0%; Score 49; DB 6; Length 250;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX RES11
 XX ADA05734 Human NOV18b protein SEQ ID NO:94.
 XX ID ADA05734 standard; protein; 252 AA.
 XX AC ADA05734;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human NOV18b protein
 XX KW; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 XX immunomodulator; cytostatic; nootropic; neuroprotective;
 XX antiparkinsonian; antilipaemic; gene therapy; human disease;
 XX metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 XX immune disorder; haematopoietic disorder; dyslipidaemia.
 XX Homo sapiens.

XX OS WO2003029424-A2.
 PN 10-APR-2003.
 XX PD 02-OCT-2002; 2002WO-US031373.
 XX PR 02-OCT-2001; 2001US-0326483P;
 PR 05-OCT-2001; 2001US-0327335P;
 PR 05-OCT-2001; 2001US-0327449P;
 PR 09-OCT-2001; 2001US-0327917P;
 PR 09-OCT-2001; 2001US-0328039P;
 PR 09-OCT-2001; 2001US-0328049P.

PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-033014P.
 PR 18-OCT-2001; 2001US-0330303P.
 PR 22-OCT-2001; 2001US-034103P.
 PR 24-OCT-2001; 2001US-034262P.
 PR 29-OCT-2001; 2001US-034957P.
 PR 01-NOV-2001; 2001US-03435P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-037381P.
 PR 19-APR-2002; 2002US-037382P.
 PR 19-APR-2002; 2002US-037388P.
 PR 22-APR-2002; 2002US-037497P.
 PR 16-MAY-2002; 2002US-038103P.
 PR 16-MAY-2002; 2002US-038103P.
 PR 16-MAY-2002; 2002US-038104P.
 PR 17-MAY-2002; 2002US-038164P.
 PR 28-MAY-2002; 2002US-038365P.
 PR 29-MAY-2002; 2002US-038383P.
 PR 25-JUN-2002; 2002US-039133P.
 PR 01-OCT-2002; 2002US-0046251L.
 XX (CURA-) CURAGEN CORP.
 XX PA Smithson G, Milliet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patrurajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Catterton E; Ort T, Gorman L, Zerhusen BD, Anderson DW,
 PI Ji W, Miller CB, Rastelli L, Stone DJ, Pera CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach ND, Agee ML, Bergs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX DR WPI; 2003-381626/36.
 XX N-PSDB; ADA05733.
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidaemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX Claim 1: Page 170; 586PP; English.
 XX
 CC The present invention describes NOVX Proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX Protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide described above; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating a
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipaemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 XX present invention.

SQ Sequence 252 AA;
 Query Match 100.0%; Score 49; DB 6; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KMNEYTVHL 9
 Db 71 KMNEYTVHL 79

RESULT 12
 AAR67888 standard; protein; 253 AA.
 XX
 AC AAR67888;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-AUG-1995 (first entry)
 XX Human stratum corneum chymotrophic recombinant enzyme (SCCE).
 DE
 XX Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
 KW callosities; keratosis pilaris; ichthyoses; eczema.
 XX Homo sapiens.
 OS
 PN W09500651-A1.
 XX
 PD 05-JAN-1995.
 XX
 PF 20-JUN-1994; 94WO-IB000166.
 XX
 PR 18-JUN-1993; 93DK-00000725.
 XX
 PA (SYMB-) SYMBIOTIC AB.
 XX
 PI Egelrud T, Hansson L;
 XX
 DR 1995-052088/07.
 DR N-NSDB; AAQ81203.

XX Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
 PT related vectors, transformed cells and polypeptides, useful for treating
 PT skin disorders, e.g. acne or psoriasis, and for identification of
 PT specific inhibitors.
 XX Disclosure: Page 97; 137pp; English.

CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
 CC and skin care products, especially to treat and prevent acne, xerosis,
 CC or other hyperkeratotic conditions (e.g. callousness or keratosis
 CC pilaris), ichthyoses, psoriasis, etc. It is produced
 CC recombinantly following mammal, insect, plant, or microorganism
 CC transformation with plasmid PS507. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX Sequence 253 AA;

SQ Query Match 100.0%; Score 49; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KMNEYTVHL 9
 Db 72 KMNEYTVHL 80

RESULT 13
 AAW05383 standard; protein; 253 AA.
 ID AAW05383;
 XX
 AC AAW05383;
 XX
 DT 31-DBC-1996 (first entry)
 XX Human amyloid precursor protein protease.
 DB Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09631122-A1.
 XX
 PD 10-OCT-1996.
 XX
 PF 02-APR-1996; 96WO-US004294.
 XX
 PR 04-APR-1995; 95US-00416257.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Dixon EP, Johnstone EM, Little SP;
 XX
 DR WPI; 1986-46694/46.
 DR N-PSDB; AAT3783.
 XX
 PT New isolated human amyloid precursor protein protease - used to develop
 PT prods. for the treatment or diagnosis of associated conditions, esp.
 PT Alzheimer's disease.
 XX
 PS Claim 1; Page 44-45; 55pp; English.
 XX
 CC Human amyloid precursor protein protease (AAW05383) is involved in the
 CC processing or clearance of amyloid precursor protein to form beta-amyloid
 CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAW05383)
 CC obt'd. from a human lung library. Recombinant Protease can be produced in
 CC transfected or transfected prokaryotic (partic E. coli) or eukaryotic
 CC (partic. AV-120 host cells. It is used to develop prods. for the design
 CC and testing of prods. useful for treating or preventing conditions
 CC associated with beta-amyloid peptide, esp. Alzheimer's disease
 XX
 SQ Sequence 253 AA;

Query Match 100.0%; Score 49; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KMNEYTVHL 9
 Db 72 KMNEYTVHL 80

RESULT 14
 ABBB4421 standard; peptide; 253 AA.
 ID ABBB4421.
 AC
 XX
 AC ABBB4421;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Human SCCE protein N-terminal fragment SEQ ID 48.
 XX
 SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
 KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
 KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
 KW pruritis; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
 XX
 OS Homo sapiens.

XX PN Homo sapiens.
 XX OS
 PN WO200262135-A2.
 XX XX
 PD 15-AUG-2002.
 XX XX
 PP 08-FEB-2002; 2002WO-TB001300.
 XX PR 09-FEB-2001; 2001CA-02332655.
 XX PR 09-FEB-2001; 2001DK-00000218.
 PA (EGEL,) EGELRUD T.
 PA (HANS,) HANSSON L.
 PA (HANS//) HANSSON L.
 XX DR
 PI Egelrud T, Hansson L;
 XX WPI: 2002-643380/69.
 PT DR N-PSDB; ABQ76226.
 PT XX
 PT Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
 PS PT
 PS PT
 PS Example 6; Page 37; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous SCCE or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for improving treatment, to relieve pruritis, atopic dermatitis, acne and inherited skin diseases selected from diseases consisting of epidermal hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritis, atopic dermatitis, eczema, acne and inherited skin diseases selected from diseases consisting of epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the N-terminal fragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KK7), used in the development of the transgenic mammals described in the invention
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 49; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Sequence 253 AA;
 SQ Query Match 100.0%; Score 49; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KNEYTVHL 9
 Db 72 KNEYTVHL 80
 RESULT 15
 ID ABB84406 standard; protein: 253 AA.
 AC ABB84406;
 XX DT 08-NOV-2002 (first entry)
 DE Human SCCE protein.
 XX XX
 KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
 KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
 KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
 KW pruritis; atopic dermatitis; eczema; itch; KK7; enzyme
 KW KW

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:21:01 ; Search time 10.2222 Seconds
 (without alignments)
 84.690 Million cell updates/sec

Title: US-09-905-083-31
 Perfect score: 49
 Sequence: 1 KMNEYTVHL 9
 Scoring table: GapOp 10.0 , Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR78;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	49	100.0	253	2	AS5968		serine protease
2	39	79.6	218	1	YVBPK3		lysis protein t -
3	39	79.6	218	1	YVBP74		lys protein t -
4	37	75.5	334	2	B90019		conserved hypothetical
5	37	75.5	393	2	D75207		hypothetical prote
6	36	73.5	627	2	T35395		hypothetical prote
7	36	73.5	1829	2	T34239		hypothetical prote
8	35	71.4	159	2	A11406		spermidine/spermine
9	35	71.4	159	2	A11482		spermidine/spermine
10	35	71.4	505	2	H75431		conserved hypothetical
11	35	71.4	555	2	AD1794		acylase and diester
12	34	71.4	667	2	T09482		ring finger protein
13	35	71.4	667	2	T09013		ring finger protein
14	34	69.4	270	2	A43711		replication protein
15	34	69.4	270	2	S28682		replication protein
16	34	69.4	285	2	F7048		hypothetical prote
17	34	69.4	421	2	AC1481		conserved hypothetical
18	34	69.4	421	2	AK1120		B. subtilis YubN p
19	33	67.3	204	2	B31227		nitrogen fixation
20	33	67.3	204	2	E95345		FixJ Transcription
21	33	67.3	218	2	S53154		calflegin Tb-24 -
22	33	67.3	218	2	E83724		hypothetical prote
23	33	67.3	227	2	D83796		two-component resp
24	33	67.3	53155	2			calflegin Tb-1.7 -
25	33	67.3	233	1	AQ717		flagellar calcium-
26	33	67.3	407	2	S53153		flagelin Tb-4A -
27	33	67.3	422	2	T11714		hypothetical prote
28	33	67.3	429	2	H70307		preprotein translo
29	33	67.3	525	2	B84028		olopeptide ABC t

ALIGNMENTS

hypothetical protein	30	33	67.3	664	2	C72379
TnB-dependent rec	31	33	67.3	677	2	A87470
pyrL3 protein - s	32	33	67.3	1042	2	S23738
probable membrane	33	33	67.3	1308	2	E71622
Pyrimidine synthet	34	33	67.3	1481	1	OZDOP3
50S ribosomal prot	35	32	65.3	49	2	H89908
hypothetical prote	36	32	65.3	84	2	AE2172
ribosomal protein	37	32	65.3	116	2	S24989
hypothetical prote	38	32	65.3	130	2	E97262
hypothetical prote	39	32	65.3	144	2	F71215
Mdab protein homol	40	32	65.3	192	2	G81301
hypothetical prote	41	32	65.3	228	2	C90033
hypothetical prote	42	32	65.3	304	2	H75378
probable membrane-	43	32	65.3	339	2	F97121
conserved hypothetical	44	32	65.3	371	2	A89800
citrate/sodium sym	45	32	65.3	448	2	F82280

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probable membrane	33	33	67.3	1308	2	E71622
Pyrimidine synthet	34	33	67.3	1481	1	OZDOP3
50S ribosomal prot	35	32	65.3	49	2	H89908
hypothetical prote	36					

RESULT 5
 Query Match Similarity 79.6%; Score 39; DB 1; Length 218;
 Best Local Similarity 87.5%; Pred. No. 2,2; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Species: Pyrococcus abyssi (strain Orsay)
 C;Cross-references: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
 C;Accession: D75207
 R;anonymous Genoscope
 Submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
 A;Reference number: A75001
 A;Accession: D75207
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-393 <KAN>
 A;Cross-references: GB:AJ248283; GB:AL096836; NID:95457433; PIDN:CA49107.1; PID:9545761
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB2235
 C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0196

RESULT 3
 Query Match Similarity 75.5%; Score 37; DB 2; Length 393;
 Best Local Similarity 66.7%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Species: Pyrococcus abyssi (strain Orsay)
 C;Cross-references: Pyrococcus abyssi
 C;Accession: D75207
 A;Reference number: A75001
 A;Molecule type: DNA
 A;Residues: 1-218 <T4>
 A;Cross-references: GB:Y00408; NID:G15368; PIDN:CA468470.1; PID:915369
 A;Note: the sequence is almost identical with that of the E.coli phage K3
 C;Comment: At the end of the growth cycle, phage T4 expresses two genes with lysis funct
 about the gene product of t, although it has been suggested that it acts as a phospholi
 C;Genetics:
 A;Gene: t
 A;Map position: 157.985-158.639
 C;Superfamily: phage T4 lysis protein t
 C;Keywords: host cell lysis; transmembrane protein
 F:35-49/Domain: transmembrane #status predicted <TMNN>

Query Match Similarity 79.6%; Score 39; DB 1; Length 218;
 Best Local Similarity 87.5%; Pred. No. 2,2; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Species: Pyrococcus abyssi (strain Orsay)
 C;Cross-references: Pyrococcus abyssi
 C;Accession: D75207
 A;Reference number: A75001
 A;Molecule type: DNA
 A;Residues: 1-627 <WIL>
 A;Cross-references: GB:Z92813; PIDN:CA49107.1; GSPDB:GN00021; CESP:T28A8.6
 C;Genetics:
 A;Gene: CESP:T28A8.6
 A;Map position: 3
 A;Intron: 51/2; 89/2; 183/2; 221/2; 296/2; 607/3
 C;Superfamily: Caenorhabditis elegans hypothetical protein Y57A10.4

RESULT 6
 Query Match Similarity 73.5%; Score 36; DB 2; Length 627;
 Best Local Similarity 66.7%; Pred. No. 28; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Species: Caenorhabditis elegans hypothetical protein Y57A10.4
 C;Cross-references: GB:Z92813; PIDN:CA49107.1; GSPDB:GN00021; CESP:T28A8.6
 C;Accession: T25395
 R;Lloyd, C.
 Submitted to the EMBL Data Library, March 1997
 A;Reference number: Z20027
 A;Accession: T25395
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-627 <WIL>
 A;Cross-references: GB:Z92813; PIDN:CA49107.1; GSPDB:GN00021; CESP:T28A8.6
 C;Genetics:
 A;Gene: CESP:T28A8.6
 A;Map position: 3
 A;Intron: 51/2; 89/2; 183/2; 221/2; 296/2; 607/3
 C;Superfamily: Caenorhabditis elegans hypothetical protein Y57A10.4

RESULT 4
 B98019
 conserved hypothetical protein spril179 [imported] - Streptococcus pneumoniae (strain R6)
 C;Species: Streptococcus pneumoniae
 C;Accession: B98019
 R;Hoskins, J.A.; Alborn, Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Liefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 Y, P.; Sun, P.M.; Winkler, M.E.
 J.; Bacterios, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Accession: B98019
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <KUR>
 A;Cross-references: GB:AE007317; PIDN:AAK99982.1; PID:915458811; GSPDB:GN00174
 C;Genetics:
 A;Gene: spril179
 Qy 1 KMNNEYTVHL 9
 Db 302 KMNNEYTHI 310

RESULT 7
 T34239
 hypothetical protein F26F12.7 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T34239
 R;Wilson, R.; Bentley, D.; Gattung, S.
 Submitted to the EMBL Data Library, April 1996
 A;Description: The sequence of C. elegans cosmid F26F12.
 A;Reference number: Z21493
 A;Accession: T34239
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA

A;Residues: 1-1829 <NIL>
A;Cross-references: EMBL:U55373; PIDN:AAC25894.1; GSPDB:GN00023; CESP:F26F12.7
A;Experimental source: strain Bristol N2; clone F26F12
C;Genetics:
A;Gene: CESP:F26F12.7
A;Intron position: 5
A;Introns: 110/-3; 441/-3; 801/-2; 1244/-3; 1693/-2; 1784/-1

Query Match Score 73.5%; Score 36; DB 2; Length 1829;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KNEYTVH 8
Db 765 KNEYTH 771

RESULT 8
spermidine/spermine N1-acetyl transferase homolog lmo2658 [Imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Accession: AI1406
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
R;Glaeser, P.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kahn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AI1406
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:NC_003410; PIDN:CAD00871.1; PID:916412158; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2658

Query Match Score 71.4%; Score 35; DB 2; Length 159;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVH 8
Db 139 KMSEWTNH 146

RESULT 9
spermidine/spermine N1-acetyl transferase homolog lin2807 [Imported] - Listeria innocua
C;Species: Listeria innocua
C;Accession: AI1782
R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kahn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AI1782
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: 1-39 <GLA>
A;Experimental source: strain Clip11262
A;Gene: lin2807

Query Match Score 71.4%; Score 35; DB 2; Length 159;

RESULT 10
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Accession: H75431
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; S.; Smith, H.O.; Venturini, J.C.; Fraser, C.M.; Science 286, 1571-1571, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:2036896; PMID:10567266
A;Accession: H75431
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE001964; GB:AE000513; NID:96458881; PIDN:AAF10722.1; PMID:96458888;
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR150
A;Map Position: 1
C;Superfamily: conserved hypothetical protein b0835
Query Match Score 71.4%; Score 35; DB 2; Length 505;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KNEYTVH 9
Db 57 QNEYDTHL 65

RESULT 11
acylase and diesterase homolog lin2898 [Imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Accession: AD1794
R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matoh, C.; Schlüter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1794
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL592022; PIDN:CA98124.1; PMID:916415433; GSPDB:GN00178
A;Experimental source: strain Clip11262
A;Gene: lin2898

Query Match Score 71.4%; Score 35; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNEYTVH 9
Db 483 KNEYDTDL 491

RESULT 12

T09482
Ring finger protein FXY - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C;Accession: T09482
R;Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A;Description: The human FXY maps to chromosome Xp22.3: Implications for evolution of the human FXY gene. Reference number: Z16687
A;Accession: T09482
A;Molecule type: mRNA
A;Residues: 1-667 <PER>
A;Cross-references: EMBL:AF035360; NID:92827993; PID:92827994
C;Genetics:
A;Gene: FXY
A;Map position: Xp22.3
C;Superfamily: RING finger homology <RRN>
F;6/65/Domain: RING finger homology <RRN>
Query Match 71.4%; Score 35; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KMNNEYTVH 8
Db 444 KQNHYTVH 451

RESULT 13
T0913
RING finger protein FXY - mouse
C;Species: Mus musculus (house mouse)
C;Accession: T09013
R;Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A., 94, 12030-12035, 1997
A;Title: A gene spans the pseudautosomal boundary in mice.
A;Reference number: Z16531; MUID:9804518; PMID:9342357
A;Accession: T09013
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-667 <PAL>
A;Cross-references: EMBL:AF026565; NID:92589222; PID:92589223
C;Genetics:
A;Gene: FXY
A;Map position: X; Y
C;Superfamily: RING finger homology
C;Keywords: zinc finger
F;6/65/Domain: RING finger homology <RRN>

Query Match 71.4%; Score 35; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KMNNEYTVH 8
Db 444 KQNHYTVH 451

RESULT 14
A43711
replication Protein repA 32K chain - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 16-Feb-2001
C;Accession: A43711
R;Erdile, L.F.; Wold, M.S.; Kelly, T.J.
J. Biol. Chem., 265, 3177-3182, 1990
A;Title: The primary structure of the 32-kDa subunit of human replication protein A.
A;Reference number: A43711; MUID:10153966; PMID:2406247
A;Accession: A43711
A;Status: Preliminary
A;Molecule type: mRNA

Result No.	Score	Query Match Length	DB ID	Description
1	49	100.0	9	US-09-918-243-31 Sequence 31, Appl
2	49	100.0	9	US-09-918-243-89 Sequence 89, Appl
3	49	100.0	9	US-09-918-243-109 Sequence 109, Appl
4	49	100.0	9	US-09-905-083-31 Sequence 31, Appl
5	49	100.0	9	US-09-905-083-89 Sequence 89, Appl
6	49	100.0	9	US-09-905-083-109 Sequence 109, Appl
7	49	100.0	144	US-09-756-294-44 Sequence 4, Appl
8	49	100.0	144	US-10-161-78-4 Sequence 4, Appl
9	49	100.0	253	US-09-838-615-98 Sequence 98, Appl
10	49	100.0	253	US-09-754-752-3 Sequence 3, Appl
11	49	100.0	253	US-10-284-283-90 Sequence 90, Appl
12	49	100.0	253	US-10-395-021-498 Sequence 498, Appl
13	49	100.0	253	US-10-173-991-48 Sequence 48, Appl
14	39	79.6	9	US-09-918-243-122 Sequence 122, Appl
15	39	79.6	9	US-09-905-083-122 Sequence 122, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Query Match Length DB ID

Result No.	Score	Query Match Length	DB ID	Description
1	49	100.0	9	US-09-918-243-31 Sequence 31, Appl
2	49	100.0	9	US-09-918-243-89 Sequence 89, Appl
3	49	100.0	9	US-09-918-243-109 Sequence 109, Appl
4	49	100.0	9	US-09-905-083-31 Sequence 31, Appl
5	49	100.0	9	US-09-905-083-89 Sequence 89, Appl
6	49	100.0	144	US-09-756-294-44 Sequence 4, Appl
7	49	100.0	144	US-10-161-78-4 Sequence 4, Appl
8	49	100.0	253	US-09-838-615-98 Sequence 98, Appl
9	49	100.0	253	US-09-754-752-3 Sequence 3, Appl
10	49	100.0	253	US-10-284-283-90 Sequence 90, Appl
11	49	100.0	253	US-10-395-021-498 Sequence 498, Appl
12	49	100.0	253	US-10-173-991-48 Sequence 48, Appl
13	49	100.0	253	US-09-918-243-122 Sequence 122, Appl
14	39	79.6	9	US-09-905-083-122 Sequence 122, Appl
15	39	79.6	9	US-09-905-083-122 Sequence 122, Appl

OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-31

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 2

US-09-918-243-89

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO: 31

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 3

US-09-918-243-31

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO: 31

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 4

US-09-918-243-89

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO: 31

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 5

US-09-918-243-89

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO: 31

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 6

US-09-918-243-89

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO: 31

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 7

US-09-918-243-89

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO: 31

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: US-09-918-243-31

Query Match Score 49; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9

Db 1 KMNEYTVHL 9

RESULT 8

US-09-918-243-89

Sequence 89, Application US/09918243

Patent No. US20142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

CANNON, Martin J.

SANTIN, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

FILE REFERENCE: D6223CIP/C/DCIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

APPLICANT: O'Brien, Timothy J.
 APPLICANT: Cannon, Martin J.
 APPLICANT: Santin, Alessandro
 TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D6223CIP/C/D/CIP
 CURRENT APPLICATION NUMBER: US/09/918,243
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US
 PRIOR FILING DATE: 2001-07-13
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 89
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 72-80 of the SCCE protein
 US-09-918-243-89

Query Match Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Prod. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNETVHL 9
 Db 1 KNNETVHL 9

RESULT 3
 US-09-918-243-109
 Sequence 109, Application US/09918243
 Patent No. US20020142317A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Cannon, Martin J.
 APPLICANT: Santin, Alessandro
 TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D6223CIP/C/D/CIP
 CURRENT APPLICATION NUMBER: US/09/918,243
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/918,243
 PRIOR FILING DATE: 2001-07-30
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 109
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 72-80 of the SCCE protein
 US-09-918-243-109

Query Match Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Prod. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNETVHL 9
 Db 1 KNNETVHL 9

RESULT 4
 US-09-905-083-31
 Sequence 31, Application US/09905083
 Patent No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 FILE REFERENCE: D6223CIP/C/DIV
 CURRENT APPLICATION NUMBER: US/09/905,083
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US/09/502,600
 SEQ ID NO: 109
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 72-80 of the SCCE protein

PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 31
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 72-80 of the SCCE protein
 US-09-905-083-31

Query Match Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Prod. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNETVHL 9
 Db 1 KNNETVHL 9

RESULT 5
 US-09-905-083-89
 Sequence 89, Application US/09905083
 Patent No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 FILE REFERENCE: D6223CIP/C/DIV
 CURRENT APPLICATION NUMBER: US/09/905,083
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US/09/502,600
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 89
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 72-80 of the SCCE protein
 US-09-905-083-89

Query Match Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Prod. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNNETVHL 9
 Db 1 KNNETVHL 9

RESULT 6
 US-09-905-083-109
 Sequence 109, Application US/09905083
 Patent No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 FILE REFERENCE: D6223CIP/C/DIV
 CURRENT APPLICATION NUMBER: US/09/905,083
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US/09/502,600
 SEQ ID NO: 109
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 72-80 of the SCCE protein

Query Match 100.0%; Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVHL 9
 Db 1 KNEYTVHL 9

RESULT 7
 US-09-796-294-4
 Sequence 4, Application US/09796694
 ; Patent No. US2002003751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; TITLE OF INVENTION: Extracellular Serine Protease
 ; FILE REFERENCE: D6020CIP3
 ; CURRENT APPLICATION NUMBER: US/09/796,294
 ; PRIORITY FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US 09/618,259
 ; PRIOR FILING DATE: 2000-07-18
 ; SEQ ID NO: 4
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: unknown
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
 ; OTHER INFORMATION: enzyme (scce) catalytic domain
 US-09-796-294-4

Query Match 100.0%; Score 49; DB 9; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.086%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVHL 9
 Db 9 KNEYTVHL 17

RESULT 8
 US-10-461-787-4
 Sequence 4, Application US/10461787
 ; Publication No. US201030199010A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; TITLE OF INVENTION: No. US201030199010A1 Extracellular Serine Protease
 ; FILE REFERENCE: D6020CIP2
 ; CURRENT APPLICATION NUMBER: US/10/461,787
 ; CURRENT FILING DATE: 2003-06-13
 ; PRIOR APPLICATION NUMBER: US/09/618,259
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: US 09/127,444
 ; PRIOR FILING DATE: 1998-08-21
 ; SEQ ID NO: 4
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: unknown
 ; NAME/KEY: DOMAIN
 ; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
 US-10-461-787-4

Query Match 100.0%; Score 49; DB 14; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.086%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVHL 9
 Db 9 KNEYTVHL 17

RESULT 9
 US-09-988-615-98
 Sequence 9, Application US/09888615
 ; Patent No. US20020064851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOWMAN, GREGORY
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: CENEPEP, SEAN
 ; APPLICANT: CHARYDZAK, GLEN
 ; APPLICANT: MANNING, GERARD
 ; APPLICANT: SUDARSHANAM, SUCHA
 ; TITLE OF INVENTION: NOVEL PROTEASES
 ; FILE REFERENCE: 038602/1214
 ; CURRENT APPLICATION NUMBER: US/09/888,615
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: 60/214,047
 ; PRIOR FILING DATE: 2000-06-26
 ; NUMBER OF SEQ ID NOS: 150
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 98
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-988-615-98

Query Match 100.0%; Score 49; DB 9; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.15%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNEYTVHL 9
 Db 72 KNEYTVHL 80

RESULT 10
 US-09-764-764-3
 Sequence 3, Application US/09764762
 ; Patent No. US20020068341A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; Lal, Preeti
 ; TITLE OF INVENTION: NOVEL KALLIKEIN
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: PatentSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/764,762
 ; FILING DATE: 16-Jan-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/210,084
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0252 US
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 532504
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-764-762-3

Query Match 100.0%; Score 49; DB 9; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.15%; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Qy 1 KRMNEYTVHL 9
 Db 72 KRMNEYTVHL 80

RESULT 11
 US-10-264-283-90
 Sequence 90, Application US/10264283
 Publication No. US2003014494A1
 GENERAL INFORMATION:
 APPLICANT: Algec, Paul A.
 APPLICANT: Mannion, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 21:0121_590
 CURRENT APPLICATION NUMBER: US/10/264,283
 CURRENT FILING DATE: 2002-10-02
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: Corixa Invention Disclosure Database
 SEQ ID NO 90
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-264-283-90

Query Match 100.0%; Score 49; DB 14; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.15%; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Qy 1 KRMNEYTVHL 9
 Db 72 KRMNEYTVHL 80

RESULT 12
 US-10-295-027-498
 Sequence 498, Application US/10295027
 Publication No. US200302350A1
 GENERAL INFORMATION:
 APPLICANT: Afar, Daniel
 APPLICANT: Aziz, Natasha
 APPLICANT: Ginsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Bos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 498
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-498

Query Match 100.0%; Score 49; DB 15; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.15%; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Qy 1 KRMNEYTVHL 9
 Db 72 KRMNEYTVHL 80

RESULT 13
 US-10-173-99-48
 Sequence 48, Application US/10173999
 Publication No. US20040005563A1
 GENERAL INFORMATION:
 APPLICANT: Mack, David H.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Bos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions and Methods of Screening for Modulators of Ovarian Cancer
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 01B501-002420US
 CURRENT APPLICATION NUMBER: US/10/173,999
 CURRENT FILING DATE: 2002-06-17
 PRIOR APPLICATION NUMBER: US 60/299,234
 PRIOR FILING DATE: 2001-06-18
 PRIOR APPLICATION NUMBER: US 60/315,287
 PRIOR FILING DATE: 2001-08-27
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/372,246
 PRIOR FILING DATE: 2001-04-12
 NUMBER OF SEQ ID NOS: 163
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 48
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-173-99-48

Query Match 100.0%; Score 49; DB 15; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.15%; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Qy 1 KRMNEYTVHL 9

Db 72 KNEYTVHL 80

RESULT 14
 US-09-918-243-122
 Sequence 122; Application US/09918243
 Patent No. US2002014231A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Cannon, Martin J.
 APPLICANT: Santini, Alessandro
 TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D6223CIP/C/D/CIP
 CURRENT APPLICATION NUMBER: US/09/918,243
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US
 PRIOR FILING DATE: 2001-07-13
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO 122
 LENGTH: 9
 TYPE: PRT
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 74-82 of the SCCE protein
 US-09-918-243-122

Query Match 79.6%; Score 39; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 NEYTVHL 9
 Db 1 NEYTVHL 7

RESULT 15
 US-09-905-083-122
 Sequence 122; Application US/09905083
 Patent No. US20020146708A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 FILE REFERENCE: D6223CIP/C/DIV
 CURRENT APPLICATION NUMBER: US/09/905,083
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 09/502,600
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO 122
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 74-82 of the SCCE protein
 US-09-905-083-122

Query Match 79.6%; Score 39; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 NEYTVHL 9
 Db 1 NEYTVHL 7

Search completed: March 1, 2004, 18:08:48
 Job time : 25.1111 secs

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```

[1] SEQUENCE FROM N.A.
RP MEDLINE=87250254; PubMed=3597316;
RA Riede T. ;
RT "Lysis gene t of T-even bacteriophages: evidence that colicins and
bacteriophage genes have common ancestors.";
RL J. Bacteriol. 169:2956-2961(1987).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M16812; AAA88A15.1; -
DR PIR: A27093; YVBPK3.
KW Phage lysis protein; MW: 21B4DC02ACA0ECF6 CRC64;
SQ SEQUENCE 218 AA; 25222 MW; 21B4DC02ACA0ECF6 CRC64;
Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 MNEYYVHL 9
Db 139 MDEYYVHL 146

RESULT 3
VLYS_BPT4 STANDARD; PRT; 218 AA.
ID P06805;
AC P06805;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lysis protein (Holin) (Protein rv).
GN T OR RV.
OS Bacteriophage T4.
OC Virus; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OX NCBI_TAXID:106655;
RN SEQUENCE FROM N.A.
RP MEDLINE=87316934; PubMed=35628006;
RA Montag D., Degen M., Henning U. ;
RT "Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4." ;
PL Nucleic Acids Res. 15:6736-6736(1987).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=88011333; PubMed=12626685;
RA Miller E.S., Kutter E., Mosig G., Ariasaka F., Kunisawa T., Ruger W. ;
RT "Bacteriophage T4 genome." ;
PL Microbiol. Mol. Biol. Rev. 67:86-156 (2003).
RN [3]
RN SEQUENCE OF 1-34 FROM N.A.
RP MEDLINE=88011336; PubMed=2958637;
RA Montag D., Riede I., Eschbach M.-L., Degen M., Henning U. ;
RT "Receptor-recognizing Proteins of T-even type bacteriophages.
RT Constant and hypervariable regions and an unusual case of
RT evolution." ;
PL J. Mol. Biol. 196:165-174 (1987).
RN SEQUENCE OF 202-218 FROM N.A.
RP STRAIN=D;
RC MEDLINE=93106978; PubMed=8416914;
RA Orsini G., Ouhammouche M., le Caer J.P., Brody E.N./
RT "The aspa gene of bacteriophage T4 codes for the anti-sigma 70
protein";
PL J. Bacteriol. 175:85-93 (1993).
CC -----
CC -i- FUNCTION: At the end of the growth cycle, phage T4 expresses two
CC genes with lysis function. e and t. Norling is known about the

```


KW	Complete proteome.		
SQ	SEQUENCE 393 AA; 45485 MW; 9448642FBB3FBP43 CRC64;		
	Score 37; DB 1; Length 393;		
	Best Local Similarity 75.5%; Pred. No. 5.2;		
	Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
Qy	1 KMNEYTVHL 9		
Db	129 KLPXTIHL 137		
RESULT 6			
MIDI_HUMAN	ID: MID1_HUMAN STANDARD; PRT; 667 AA.		
AC	O13344; O75361; Q8ZBX5;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Midline 1 protein (Tripartite motif protein 18) (Putative transscript factor XPRF).		
DE	MIDI OR FXY OR TRINIS OR XPRF.		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC			
NCBI_TaxID=9606;			
RN [1]	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT OS-I MET-458 DEL AND PHE-ILE-ASP-SPR-GLY-ARG-HIS-LEU-534 INS.		
RP	RC TISSUE=Neuron; MEDLINE=98016411; PubMed=9354791;		
RX	Quaderi N., Schweiiger S., Gaudenz K., Franco B., Rugarli E.I., Berger W., Feldman G.J., Voita M., Andolfi G., Gilgenkrantz S., Marion R.W., Hennekam R.C.M., Opitz J.M., Ropers H.H., Ballabio A.; "Opitz GBBB syndrome, a defect of midline development, is due to mutations in a new RING finger gene on Xp22."; Nat. Genet. 17:285-291(1997).		
RN [2]	SEQUENCE FROM N.A. (ISOFORM 1).		
RP	RC TISSUE=Placenta; MEDLINE=98087583; PubMed=945238;		
RX	Perry J., Feather S., Smith A., Palmer S., Ashworth A.; "The human FXY gene is located within Xp22.3: implications for evolution of the mammalian X chromosome."; Hum. Mol. Genet. 7:299-305(1998).		
RN [3]	SEQUENCE FROM N.A. (ISOFORM 1).		
RP	RC TISSUE=Brain; MEDLINE=98390188; PubMed=9722948;		
RX	Van den Veyver I.B., Cormier T.A., Jurecic V., Baldini A., Zoghbi H.Y.; "Characterization and physical mapping in human and mouse of a novel RING finger gene in Xp22."; Genomics 51:231-261(1998).		
RN [4]	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT OS-I PRO-626.		
RP	RC TISSUE=Brain; MEDLINE=0485428; PubMed=11030761;		
RX	Suthers G.K.; "New mutations in MIDI provide support for loss of function as the cause of X-linked opitz syndrome."; Hum. Mol. Genet. 9:2553-2562(2000).		
RN [5]	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RP	MEDLINE=1231161; PubMed=1131580;		
RX	Reymond A., Meroni G., Fanozzi A., Merla G., Cairo S., Iuzi L., Riganelli D., Zanari E., Messali S., Cainarca S., Guffanti A., Minucci S., Pellicci P.G., Ballabio A.; "The tripartite motif family identifies cell compartments."; EMBO J. 20:2110-2111(2001).		
RN [6]			
	SEQUENCE FROM N.A. (ISOFORM 1).		
PC	TISSUE=Skin; MEDLINE=2388557; PubMed=12477932;		
RX	Klaunzer R.D., Collins P.S., Wagner L., Shemesh C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zabeck B., Buetow K.H., Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carrinchi P., Brange C., Bouffard G.G., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Sodergren E.J., Garcia A.M., Gay L.J., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Sanchez A., Fahey J., Hellcon E., Keittman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarh A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN [7]	INTERACTION WITH IGBP1, AND PHOSPHORYLATION.		
RP	Short K.M., Hopwood B., Yi Z., Cox T.C.; PMID=11806732;		
RX	"MIDI and MID2 homo- and heterodimerise to tether the rapanycin-sensitive PP2A regulatory subunit, APIP, to microtubules: implications for the clinical variability of X-linked Opitz GBBB syndrome and other developmental disorders."; PMID=96386064; PubMed=9718340;		
RX	Gaudenz K., Roessler E., Quaderi N., Franco B., Feldman G., Gassner D.L., Wittwer B., Horst J., Montini E., Opitz J.M., Ballabio A., Muenke M.; "Opitz GBBB syndrome in Xp22: mutations in the MIDI gene cluster in the carboxy-terminal domain"; Am. J. Hum. Genet. 63:703-710(1998).		
RN [8]	VARIANTS OS-I ARG-266 AND THR-536.		
RP	RNA Short K.M., Hopwood B., Yi Z., Cox T.C.; PMID=96386064; PubMed=9718340;		
RX	Gaudenz K., Roessler E., Quaderi N., Franco B., Feldman G., Gassner D.L., Wittwer B., Horst J., Montini E., Opitz J.M., Ballabio A., Muenke M.; "Opitz GBBB syndrome in Xp22: mutations in the MIDI gene cluster in the carboxy-terminal domain"; Am. J. Hum. Genet. 63:703-710(1998).		
RN [9]	ERRATUM.		
RP	RNA Gaudenz K., Roessler E., Quaderi N., Franco B., Feldman G., Gassner D.L., Wittwer B., Horst J., Montini E., Opitz J.M., Ballabio A., Muenke M.; "Opitz GBBB syndrome in Xp22: mutations in the MIDI gene cluster in the carboxy-terminal domain"; Am. J. Hum. Genet. 63:1571-1571(1998).		
CC	-!- FUNCTION: Putative transcriptional regulator.		
CC	-!- SUBUNIT: Homodimer or heterodimer with MID2. Interacts with IGBP1.		
CC	-!- SUBCELLULAR LOCATION: Nuclear (Probable).		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2; Name=i; Synonyms=Alpha; IsoID=O15344-1; Sequence=Displayed; Name=j; Synonyms=Beta; IsoID=O15344-2; Sequence=VSP_005735;		
CC	-!- TISSUE SPECIFICITY: In the fetus, highest expression found in kidney, followed by brain and lung. Expressed at low levels in fetal liver. In the adult, most abundant in heart, placenta and brain.		
CC	-!- DISEASE: Defects in MIDI are the cause of Opitz syndrome type I (OS-I) [MIM:300001]. OS-I is an X-linked recessive disorder characterized by hypertelorism, genital-urinary defects such as hypospadias in males and spayed labia in females, lip-palate-laryngotracheal clefts, imperforate anus, developmental delay and congenital heart defects.		
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.		
CC	-!- SIMILARITY: Contains 1 B box-type zinc finger.		
CC	-!- SIMILARITY: Contains 1 fibronectin type III domain.		
CC	-!- SIMILARITY: Contains 1 SPRY domain.		
CC	This SWISS-PROT entry is Copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -		

	Best Local Similarity Matches	Conservative Matches	Pred. No.	23;	Indels	0;	Gaps	0;	SEQUENCE	667 AA;	75210 MW;	BA73528FEE59603 CRC64;
OY	1	KNNETYVH 8							Query	1 KNNETYVH 8		
Db	444	KQNHYTVH 451							Db	444 KQNHYTVH 451		
RESULT 8												
MID1_RAT												
ID	MID1_RAT	STANDARD;	PRT;	667 AA.								
AC	P84458;											
DT	28-FEB-2003	(Rel. 41, Created)										
DT	15-MAR-2004	(Rel. 43, Last annotation update)										
DE	Midline 1 protein (Tripartite motif protein 18).											
GN	MIDI OR FXY OR TRIM18.											
OS	Rattus norvegicus (Rat).											
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.											
OX	NCBI_TaxID=10116;											
RN	[1]											
RP	SEQUENCE FROM N.A.; PubMed=943873;											
RX	Medline=943873; PubMed=10508587;											
RA	Perry J.; Ashworth A.;											
RT	"Evolutionary rate of a gene affected by chromosomal position."											
RL	Curr. Biol. 9:987-989(1999).											
CC	-!- SUBUNIT: Homodimer or heterodimer with MID2. Interacts with IGBP1 (BY SIMILARITY).											
CC	-!- SUBCELLULAR LOCATION: Nuclear (Probable).											
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.											
CC	-!- SIMILARITY: Contains 1 B-box-type zinc finger.											
CC	-!- SIMILARITY: Contains 1 SPRY domain.											
CC	-!- SIMILARITY: Contains 1 SPRY domain.											
CC	-----											
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CC	-----											
DR	EMB1; AF086461; ADD56247.1; -.											
DR	InterPro; IPD001870; B302.											
DR	DR; PRO03649; BBox_C.											
DR	InterPro; IPR008957; FN_III-like.											
DR	InterPro; IPD003961; FN_III.											
DR	DR; PRO03574; PRY.											
DR	InterPro; IPR003877; SPRY_receptor.											
DR	InterPro; IPR000315; Znf_Box.											
DR	InterPro; IPR001941; Znf_ring.											
DR	PFam; PF00041; fn1; 1.											
DR	PFam; PF00622; SPRY; 1.											
DR	PFam; PF00643; zf-B_box; 2.											
DR	PFam; PF00977; zf_C3HC4; 1.											
DR	SMART; SMART; SN00503; BBC1.											
DR	SMART; SN00336; BROX; 2.											
DR	SMART; SN00060; FN3; 1.											
DR	SMART; SN00589; PRY; 1.											
DR	SMART; SN00184; RING; 1.											
DR	SMART; SN00449; SPRY; 1.											
DR	PROSITE; PS550119; ZF_BBOX; 1..											
DR	PROSITE; PS00518; ZF_RING; 1..											
DR	PROSITE; PS550089; ZF_RING; 2..											
KW	Transcription regulation; Nuclear protein; Coiled coil; Zinc-finger; Metal-binding.											
KW	RING-TYPE.											
FT	ZN_FING 10 60											
FT	ZN_FING 170 212											
FT	DOMAIN 205 264											
FT	DOMAIN 384 477											
FT	DOMAIN 538 657											

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CC	DR	EMBL: Y14848; CBA75113_1; -.	RL	Hum. Mol. Genet. 8:1397-1407(1999).
CC	DR	MGD: MGI:1100537; Midori.	CC	[2] SEQUENCE FROM N.A.
CC	InterPro	IPR001870; B302.	RP	SEQUENCE ID: PubMed=10644436;
CC	InterPro	IPR003649; Bbox_C-like.	RA	PERRY J., Short K.M., Romer J.T., Swift S., Cox T.C., Ashworth A.;
CC	InterPro	IPR008957; FN_III-like.	RT	"FXY2/MID2, a gene related to the X-linked Opitz syndrome gene
CC	InterPro	IPR003961; FN_III.	RT	FXY2/MID2 maps to Xq22, and encodes a FNIII domain-containing protein
CC	InterPro	IPR003877; SPRY_receptor.	RT	that associates with microtubules.";
CC	InterPro	IPR000315; Znf_Ebox.	Genomics 62:185-194 (1999).	
CC	InterPro	IPR000384; Znf_ring.	-!- SUBUNIT: Homodimer or heterodimer with MID1. Interacts with ICBP1	
CC	PFam	PF000041; fn3; 1.	(By similarity).	
CC	PFam	PF00622; SPRY; 1.	-!- SUBCELLULAR LOCATION: Cyttoplasmic; microtubule-associated.	
CC	PFam	PF00643; zf-B_box; 2.	-!- TISSUE SPECIFICITY: Low abundance in brain and lung, with even	
CC	PFam	PF000037; zf-C3HC4; 1.	lower levels in heart, liver, and kidney.	
CC	SMART	SM00502; BBC; 1.	-!- DEVELOPMENTAL STAGE: At P10.5, a very low level is mostly confined	
CC	SMART	SM00336; BBOX; 2.	to the central nervous system and the developing heart and kidney,	
CC	SMART	SM00060; FN3; 1.	while at later stages it is present in other organ systems.	
CC	SMART	SM00184; RING; 1.	-!- DOMAIN: The tripartite motif (RBCC; RING; Zinc-finger)	
CC	SMART	SM00449; SPRY; 1.	fingers and coiled coil domains) mediates dimerization (By	
CC	PROSITE	PS00119; ZF_BBOX; 1.	similarity).	
CC	PROSITE	PS00518; ZF_RING; 1; 1.	-!- DOMAIN: Associates with microtubules in a manner that is dependent	
CC	PROSITE	PS00089; ZF_RING; 1; 1.	on the C-terminal B30.2 domain.	
CC	PROSITE	ZN_FINGER; Alternative splicing.	-!- PTM: Phosphorylated on serine and threonine residues (By	
KW	METAL_BINDING	Zinc-finger; Zinc-finger; Zinc-finger;	similarity).	
FT	ZN_FINGER	10 60	-!- SIMILARITY: Belongs to the TRIM/RBCC family.	
FT	ZN_FINGER	170 212	-!- SIMILARITY: Contains 1 B-like domain.	
FT	DOMAIN	205 264	-!- SIMILARITY: Contains 2 B box-type zinc fingers.	
FT	DOMAIN	384 490	-!- SIMILARITY: Contains 1 fibronectin type III domain.	
FT	DOMAIN	551 669	-!- SIMILARITY: Contains 1 coiled coil domain.	
FT	VARSPLIC	429 442	-!- SIMILARITY: Contains 1 RING-type zinc finger.	
FT	CONFLICT	174 174	This SWISS-PROT entry is copyright. It is produced through a collaboration	
FT	CONFLICT	523 523	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
FT	CONFLICT	633 633	the European Bioinformatics Institute. There are no restrictions on its	
SQ	SEQUENCE	680 AA; 76121 MW; A9CE514A0PF7802 CRC64;	use by non-profit institutions as long as its content is in no way	
Query Match	1	KONEVTVH 8	modified and this statement is not removed. Usage by and for commercial	
Best Local Similarity	71.4%	Score 35; DB 1; Length 680;	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
Matches	75.0%	Pred. No. 24; Indels 0; Gaps 0;	or send an email to license@isb-sib.ch).	
Qy	457	KQNHYTVH 464	CC	
Db			EMBL: Y14881; CA56170.1; -.	
			EMBL: MGI:1344333; Mid2.	
			InterPro: IPR001070; B302.	
			InterPro: IPR003649; Bbox_C.	
			InterPro: IPR003861; FN_III.	
			InterPro: IPR00857; FN_III-like.	
			InterPro: IPR003877; SPRY_receptor.	
			InterPro: IPR00015; Znf_Box.	
			InterPro: IPR001841; Znf_zing.	
			PFam: PF00041; FN3; 1.	
			PFam: PF00622; SPRY; 1.	
			PFam: PF00643; zf-B_box; 1.	
			PFam: PF00097; zf-C3HC4; 1.	
			SMART: SM00502; BBC; 1.	
			SMART: SM00336; BBOX; 2.	
			SMART: SM00060; FN3; 1.	
			SMART: SM0184; RING; 1.	
			SMART: SM00449; SPRY; 1.	
			PROSITE: PS00119; ZF_BBOX; 1.	
			PROSITE: PS00518; ZF_RING; 1.	
			PROSITE: PS50089; ZF_RING; 1.	
			KW	
			Microtubule_Repeat; Coiled_coil; Metal-binding; Zinc-finger; Zinc;	
			Phosphorylation.	
			FT	
			ZN_FINGER 10 60 RING-TYPE.	
			FT	
			ZN_FINGER 114 164 B BOX-TYPE 1.	
			FT	
			ZN_FINGER 170 212 COILED_COIL (POTENTIAL).	
			FT	
			DOMAIN 208 275 FIBRONECTIN TYPE-III.	
			FT	
			DOMAIN 384 477 B30.2-LIKE.	
			FT	
			DOMAIN 486 641	
			SEQUENCE 685 AA; 77841 MW;	
			Query Match Score 71.4%; DB 1; Length 685;	
			Best Local Similarity 75.0%; Pred. No. 24; Indels 0; Gaps 0;	

RL	RN	Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases	
QY	[16]	RN	INTERACTION WITH IGBP1, AND PHOSPHORYLATION.
Db		RP	
		RX	PubMed=11806752;
		RA	"Short K.M., Hopwood B., Yi Z., Cox T.C., "MID1 and MID2 home- and heterodimerise to tether the rapanycin-sensitive PPA regulatory subunit, Alpha 4, to microtubule; implications for the clinical variability of GBBB syndrome and other developmental disorders."
		RT	
		RT	Opitz GBBS syndrome and other developmental disorders." [1]
		DT	"SUBUNIT: Homodimer or heterodimer with MID1. Interact with MID2.
		CC	"- ALTERNATIVE PRODUCTS:
		CC	"Event=Alternative splicing; Named isoforms=2; Name=1;"
		CC	"IsoId=q0UJV3-1; Sequence=Dispalyed;"
		CC	"IsoId=q0UJV3-2; Sequence=vSP_009009;"
		CC	"- TISSUE SPECIFICITY: Low level in fetal kidney and 14 adult prostate, ovary and small intestine."
		CC	"- DOMAIN: The tripartite motif (RBC: RING- fingers and coiled coil domains) mediates dimerization on the C-terminal B30.2 domain.
		CC	"- PTM: Phosphorylated on serine and threonine residues with the TRIM/RBCC family.
		CC	"- SIMILARITY: Contains 1 B30.2-like domain.
		CC	"- SIMILARITY: Contains 2 B box-type zinc fingers.
		CC	"- SIMILARITY: Contains 1 fibronectin type III domain.
		CC	"- SIMILARITY: Contains 1 RING-type zinc finger.
		CC	This SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is not removed. Usage by entities requires a license agreement (See http://www.isb-sib.ch) or send an email to licenses@isb-sib.ch).
		CC	SEQUENCE FROM N.A. (ISOFORM 2). MEDLINE=20112752; PubMed=10404436; FXY2/MID2, maps to Xq22 and encodes a PNTII domain-containing protein that associates with microtubules." [2]
		CC	SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=599330546; PubMed=10400985; Buchner G., Montali E., Andolfi G., Quaderi N., Cainarca S., Messali S., Bassi M.T., Ballabio A., Meroni G., Franco B.; "MID2, a homologue of the Opitz syndrome gene MID1: similarities in a sub-cellular localization and differences in expression during development." [3]
		CC	SEQUENCE FROM N.A. (ISOFORM 2). MEDLINE=2238257; PubMed=12477932; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Schueler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan J., Moore T., Max S.I., Wang J.J., Hsieh F., Blatchley L., Narusawa K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitman M., Madan A., Rodriquez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schinnerich A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [5]
		CC	SEQUENCE OF 1-252 FROM N.A. [6]
		CC	Health P.;
		FT	ZN FING 10 114 164
		FT	ZN FING 114 170 212
		FT	ZN FING 208 275
		RA	CORRECT CORRECT

FT	DOMAIN	384	507	FIBRONECTIN TYPE-III.
FT	DOMAIN	516	671	B30.2-LIKE.
FT	VARSPLIC	430	459	Missing (in isoform 2).
SQ	SEQUENCE	715 AA;	81233 MW;	B1051806E388BF CRC64;
Query Match		Score 35;	DB 1;	Length 715;
Best Local Similarity		71.4%;	Pred. No. 25;	
Matches		75.0%;	Mismatches 0;	
		Conservative	Indels 0;	Gaps 0;
Qy		1 KNNETTVH 8		
Db.		474 KQNHYTVH 481		
RESULT 12				
RPA2_RAT	ID=RFA2_RAT	STANDARD;	PRT;	266 AA.
AC	Q63228;			SEQUENCE FROM N.A.
DT	01-NOV-1997	(Rel. 35, Created)		TISSUE=Kidney, Lung, and Muscle;
DT	01-NOV-1997	(Rel. 35, Last sequence update)		RC MEDLINE=22388227; PubMed=12477932;
DT	01-NOV-1997	(Rel. 35, Last annotation update)		RX
DE	Replication Protein A 32 kDa Subunit (RPA-A) (RP-A)	(Replication		
DE	factor-A protein 2) (Fragment).			
GN	Rattus norvegicus	(Rat).		
OS	Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN				
RP	SEQUENCE FROM N.A.			
RA	Nageleius T., Haug T., Krokan H.E.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.			
RL	In vitro. It participates in a very early step in initiation. RP-A is a single-stranded DNA-binding protein.			
CC	-!- FUNCTION: Absolutely required for simian virus 40 DNA replication			
CC	-!- SUBUNIT: Heterotrimer of 70, 32, and 14 kDa chains. The DNA-binding activity may reside exclusively on the 70 kDa subunit.			
CC	-!- SUBCELLULAR LOCATION: Nuclear.			
CC	-!- PTM: Phosphorylation in a cell-cycle-dependent manner (from the S phase until mitosis) (By similarity).			
CC	-!- SIMILARITY: TO OTHER SPECIES RFA2/RPA2.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use, by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X98490; CAA67116; 1;			
CC	InterPro; IPR008934; Nucleic_acid_OB.			
DR	DR ID="RPA2_HUMAN"; TRNA_ant.			
DR	PRIM; PF01336; tRNA_ant; 1.			
KW	NON_TER			
FT	SEQUENCE	266 AA;	28827 MW;	52E13704C1D2E13A CRC64;
CC				
DR	Query Match	69.4%;	Score 34;	DB 1;
DR	Best Local Similarity	62.5%;	Pred. No. 14;	Length 266;
DR	Matches	Conservative	Mismatches 2;	Indels 1;
Qy		2 MNEYTVHL 9		
Db		148 : :		
RESULT 13				
RPA2_HUMAN	STANDARD;	PRT;	270 AA.	
ID	RPA2_HUMAN			
AC	P15927;			
DR	01-APR-1990 (Rel. 14, Created)			
DR	EMBL; BC01215; AAH12157; 1;			
DR	EMBL; BC001630; AAH01630; 1;			
DR	EMBL; BC021257; AAH21257; 1;			
DR	PIR; A43711; A43711;			
DR	PDB; 1DPF; 10-NUN-00.			
DR	PDB; 1LIO; 05-JUN-02.			
DR	PDB; 1QHO; 02-SEP-99.			
DR	Genew; HSGC; 10290; RPA2.			
DR	MIM; P15927; 1;			
DR	DR GO; GO:0005662; C:DNA replication factor A complex; TAS.			
DR	DR GO; GO:0003697; F:single-stranded DNA binding; TAS.			
DR	DR GO; GO:0006261; P:DNA dependent DNA replication; TAS.			
DR	InterPro; IPR008934; Nucleic_acid_OB			

InterPro; IPR004365; tRNA_anti.

DR Pfam; PF01336; tRNA_anti; 1.

KW DNA replication; Phosphorylation; Nuclear protein; 3D-structure.

FT DOMAIN 1 29 GLY/SER-RICH.

FT DOMAIN 37 45 ARG/LYS-RICH (BASIC).

FT DOMAIN 95 123 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 127 145 ARG/LYS-RICH (BASIC).

FT DOMAIN 247 270 ASP/GLU-RICH (ACIDIC).

SQ SEQUENCE 270 AA; 29247 MW; 61A563EA/B34A81I CRC64;

Query Match 69.4%; Score 34; DB 1; Length 270;

Best Local Similarity 62.5%; Pred. No. 14;

Matches 5; Conservative 2; N mismatches 1; Indels 0; Gaps 0;

Qy 2 MNEYTVHL 9

Db 152 MNEFTHI 159

RESULT 14

RFA2_MOUSE STANDARD; PRT; 270 AA.

ID RFA2 MOUSE STANDARD; PRT; 270 AA.

AC 062113; 35, Created)

DT 01-MAY-1997 (Rel. 35, Last sequence update)

DT 01-MAY-1997 (Rel. 35, Last annotation update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Replication protein A, 32 kDa subunit (RPA) (RPA) (Replication factor-A protein 2).

GN RPA2.

OS Mus musculus (Mouse).

OC Iwamatsu A., Sugiyama H.,

RT "cDNA cloning of the murine 30-kDa protein homologous to the 32-kDa subunit of human replication protein A.";

RL Nucleic Acids Res. 19:4392-4392 (1991).

CC -!- FUNCTION: Absolutely required for simian virus 40 DNA replication *in vitro*. It participates in a very early step in initiation. RPA is a single-stranded DNA-binding protein.

CC -!- SUBUNIT: Heterotrimer of 70, 32, and 14 kDa chains. The DNA-binding activity may reside exclusively on the 70 kDa subunit.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- PTM: Phosphorylated in a cell-cycle-dependent manner (from the S phase until mitosis) (By similarity).

CC -!- SIMILARITY: TO OTHER SPECIES RPA2/RPA2.

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DR D00812; BAA00693.1; -.

DR PIR; S28602; S28682.

DR MGI; MGI:1339939; Rpa2.

DR InterPro; IPR008999; Nucleic_acid_OB.

DR InterPro; IPR004365; tRNA_ant.

DR Pfam; PF01336; tRNA_anti; 1.

KW DNA replication; Phosphorylation; Nuclear protein.

SQ SEQUENCE 270 AA; 29718 MW; BFOEF88612A8011 CRC64;

Query Match 69.4%; Score 34; DB 1; Length 270;

Best Local Similarity 62.5%; Pred. No. 14;

Matches 5; Conservative 2; N mismatches 1; Indels 0; Gaps 0;

Qy 2 MNEYTVHL 9

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OM protein - protein search, using sw mode!

Run on: March 1, 2004, 17:20:41 ; Search time 30.3333 Seconds
(without alignments)

93.615 Million cell updates/sec

Title: US-09-905-083-31

Perfect score: 49

Sequence: 1 KMNEYTVHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31551B02 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	253	4 Q8N5N9	Q8N5N9 homo sapien
2	44	89.8	181	4 Q8NEV7	Q8NEV7 homo sapien
3	39	79.6	210	9 Q9G0B3	Q9G0B3 bacteriophage
4	37	75.5	334	16 Q8DPG2	Q8DPG2 streptococcus
5	36	73.5	603	10 Q8I836	Q8I836 arabidopsis
6	36	73.5	627	5 Q9XU04	Q9XU04 caenorhabditis
7	36	73.5	635	10 Q9LQW1	Q9LQW1 arabidopsis
8	36	73.5	753	16 Q8E6M8	Q8E6M8 streptococcus
9	36	73.5	753	16 Q8E174	Q8E174 streptococcus
10	36	73.5	753	16 Q8DVDO	Q8DVDO streptococcus
11	36	73.5	1829	5 Q19815	Q19815 caenorhabditis
12	35	71.4	47	11 Q810Y2	Q810Y2 mus spicile
13	35	71.4	47	11 Q802B4	Q802B4 mus platycephalus
14	35	71.4	47	11 Q802B3	Q802B3 arvicola terrestris
15	35	71.4	47	11 Q802B0	Q802B0 mastomys natalensis
16	35	71.4	47	11 Q802T7	Q802T7 mus cervicus

SEQUENCE FROM N.A.

RC TISSUE-SKIN;

RA Straubberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

CC BELONGS TO PEPTIDE FAMILY S1.

-!- SIMILARITY: (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DR Kallikrein 7 (chymotryptic, stratum corneum).

DB Homo sapiens (Human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hominidae;

OX NCBI_TAXID:9600;

RN [1]

PPR; PRT; 253 AA.
PRELIMINARY;
ID Q8N5N9;
AC Q8N5N9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DR GO; GO:0006508; P:chymotrypsin activity; IEA.
DR InterPro; IPRO0003; CYS_Ser trypsin.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00207; TRYSPC_1.
DR PROSITE; PS00240; TRYPSIN_DOMAIN.
DR PROSITE; PS00134; TRYPSIN_HIS.
DR PROSITE; PS00155; TRYPSIN_SER.
DR Hydrolease; Pro tease; Serine protease.
SQ SEQUENCE 253 AA; 27608 MW;

CRC64;
Query Match 100.0%; Score 49; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.076%;
Matches 9; Conservative 0; Mis matches 0; Indels 0; Gaps 0;

Qy	SQ	SEQUENCE	210 AA;	24348 MW;	C6FF585F9FE0DE68 CRC64;
Db	1	KNEYTVHL 9			
Db	72	KNEYTVHL 80			
RESULT 2					
Q8NFW7	Preliminary;	PRT;	181 AA.		
AC Q8NFW7;					
DT 01-OCT-2002 (T-EMBLrel. 22, Created)					
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)					
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)					
DB Homo sapiens (Human).					
OS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Cetacea; Metazoa; Primates; Primates J.A.; Catarrhini; Hominidae; Homo.					
NCBI_TAXID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Ovarian carcinoma,					
RA "Human Keilikrein 7" (KLK7) short variant mRNA from ovarian carcinoma."					
RT PRINTS; PR0722; CHMOTRYSIN.					
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.					
CC :- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.					
DR EMBL: AF411215; AND3663_1;					
DR GO:0004263; P:chymotrypsin activity; IEA.					
DR GO:0008233; F:peptidase activity; IEA.					
DR GO:0004295; F:trypsin activity; IEA.					
DR GO:000508; P:proteolysis and peptidolysis; IEA.					
DR InterPro: IPR004003; Cys_Ser_trypsin.					
DR InterPro: IPR001254; Peptidase_S1.					
DR InterPro: IPR001314; Peptidase_S1A.					
PFAM: PF00089; trypsin; 1.					
DR PRINTS; PR0722; CHMOTRYSIN.					
SMART: SM00020; TRYSPIN_1.					
PROSITE: PS50240; TRYPSIN_DOM; 1.					
PROSITE: PS00115; TRYPSIN_SER; 1.					
RW Hydrolase; Protease; Serine protease.					
SEQUENCE 181 AA; 19887 MW;					
Query Match 89.8%; Score 44; DB 4; Length 181;					
Best Local Similarity 100.0%; Pred. No. 0.57%; Indels 0; Gaps 0;					
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 2 MNEYTVHL 9					
Db 1 MNEYTVHL 8					
RESULT 3					
Q9G0B3	Preliminary;	PRT;	210 AA.		
AC Q9G0B3;					
DT 01-MAR-2001 (T-EMBLrel. 16, Created)					
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)					
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)					
DE Distal tail fiber locus, Partial sequence (Fragment).					
GN T.					
OS Bacteriophage ARI.1 viruses; no RNA stage; Caudovirales; Myoviridae; T4-like viruses.					
OC dsDNA viruses.					
OX NCBI_TAXID=66711;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=20485545; PubMed=11029414;					
RA Yu S.-L.; Ko K.-L.; Chen C.-S.; Chang Y.-C.; Syu W.-J.;					
RT "Characterization of the Distal Tail Fiber Locus and Determination of the Receptor for Phage ARI, Which Specifically Infects Escherichia coli O157:H7.";					
RT J. Bacteriol. 182:5962-5968 (2000).					
RL EMBL; AF208441; AAG29756.1;					
FT NON_TER 210					
Qy 2 MNEYTVHL 9					
Db 139 MNEYTVHL 146					
RESULT 4					
Q9DPG2	Preliminary;	PRT;	334 AA.		
AC Q9DPG2;					
DT 01-MAR-2003 (T-EMBLrel. 23, Created)					
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)					
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)					
DE Conserved hypothetical protein.					
GN SPR1179.					
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).					
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;					
OC Streptococcus.					
OC NCBI_TAXID=171101;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=21429245; PubMed=11544234;					
RA Hoskins J., Albion W.E. Jr., Arnold J., Blaszcak J.C., Burgett S., Dehoff B.S., Esrem S.T., Fritz L., Fuller D.-J., Geringer C., Gilman R., Glass J.S., Khoja H., Kraft A.R., LeBlanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matsushima P., McAhren S.M., McHenry M., McLeaster K., Mundt G.T., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rooney P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L., Glass J.I.,					
RA J. Bacteriol. 183:5709-5717 (2001).					
DR EMBL; AB008490; AAK9982.1; -.					
DR PIR: B98019; B98019.					
DR InterPro: IPR003314; DYP_perox; 1.					
DR Pfam; PF04261; DYP_perox; 1.					
DR TIGRFAM; TIGR0143; DYP_perox; 1.					
DR Hypothetical protein; Complete proteome.					
SQ SEQUENCE 334 AA; 38137 MW; E2071BC267334E5 CRC64;					
Query Match 75.5%; Score 37; DB 16; Length 334;					
Best Local Similarity 66.7%; Pred. No. 28; Indels 0; Gaps 0;					
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
Qy 1 KNEYTVHL 9					
Db 302 KNEYTVHL 310					
RESULT 5					
Q8L836	Preliminary;	PRT;	603 AA.		
AC Q8L836;					
DT 01-OCT-2002 (T-EMBLrel. 22, Created)					
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)					
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)					
DB Hypothetical protein (At1g4690).					
GN Arabidopsis thaliana (Mouse-ear cress).					
OS Euksaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
OC NCBI_TAXID=3702;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Bahn J., Carninci P., Chen H.,					

RJ	Living-lysing	Lysogenic	2012-09-27	0:
Science	28(4):2012-2018 (1998).			
EMBL	292813; CAB07289.1; -.			
DR	T28A8_1; T25395.			
DR	WormPep; T28A8_6; CE18977.			
DR	Intertaxa; IPRO00570; SPK.			
PFAM	PF04135; SPK;			
SMART	SM00583; SPK;			
SEQUENCE	627 AA; 71794 MW;	4A56E4D3658EC1CC CRC54;		
Query	Match	Similarity	Score 36;	DB 5; Length 627;
Best	Local	63.5%	DB 5;	Length 627;
Match	Conservative	66.7%	Pred. No. 86;	Tradeles
Match	Match	70.0%	2. Mismatches 1;	Tradeles

QY	1	KMNEYTVHL	9
DY	62	KMNEYSELU	70

卷之三

QILOW1	PRELIMINARY;	PRT;	635 AA.
QILOW1	AC QILOW1_0000	PRELIMINARY;	PRT; 635 AA.
QILOW1	DT 01-OCT-2000	(TREMBLrel. 15, Created)	
QILOW1	DT 01-JUN-2003	(TREMBLrel. 15, Last sequence update)	
QILOW1	DT 01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE P1066.9			
DE	Arabidopsis thaliana (Mouse-ear cress)		
DOC	Eukaryota; Viridiplantae; Streptophyta; Embryophyt		
DOC	Phylogenetic group; Magnoliophyta; eudicots; core		
DOC	eurosid I; Brassicales; Brassicaceae; Arabidopsi		
NCBI_TaxID=3702;			
[1]			
SEQUENCE FROM N.A.			
Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., K			
Williams S., Altafii H., Araujo R., Conn L., Conway			
Hansen N.F., Huizar L., Krementzkaia I., Lenz C.,			
Jurov S., Rowley D., Schwartz J., Toriumi M., Vysko			
Davis R.W., Federspiel N.A., Theologis A., Becker J			
"Genomic sequence for Arabidopsis thaliana BAC F10			
1.", Submitted (MAR-1999) to the EMBL/GenBank/DDBJ data			
[2]			
SEQUENCE FROM N.A.			
Bucher J.R.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ data			
[3]			
SEQUENCE FROM N.A.			
Bucher J.R.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ data			
[4]			
SEQUENCE FROM N.A.			
Chenck R., Shinn P., Brooks S., Buehler E., Chao Q.			
Chen S., Kim C., Altafii H., Bei B., Chin C., Chiou			
Conn L., Conway A., Gonzalez A., Hansen N., Howling			
Lee J., Lenz C., Li Gonzalez A., Liu J., Liu S., Mu			
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J.			
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis			
Theologis A., Becker J.			
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ data			
[5]			
SEQUENCE FROM N.A.			
EMBL; AC006917; AA079248; 1;			
DR InterPro; IPR07141; MAE65; ASE1.			
PFam; PF03999; MAE55; ASE1.			
SEQUENCE 635 AA; 2871C7DA1E4DA65E CR			
Query Match 73.5%; Score 36; DB 10; Length 6678; Pred. No. 87; Mismatches 2;			
Best Local Similarity 66.7%; Matches 6; Conservative 1; Mismatches 2;			
Matches 6; Conservative 1; Mismatches 2;			
Qy 1 KMNEYVHIL 9			
Db 169 KLNEYVQTHL 177			
RESULT 8			
Q8EWM8	PRELIMINARY;	PRT;	753 AA.
ID Q8EWM8	PRELIMINARY;	PRT;	753 AA.
AC	SEQUENCE FROM N.A.		
DT 01-MAR-2003	(TREMBLrel. 23, Created)		
DT 01-MAR-2003	(TREMBLrel. 23, Last sequence update)		
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DB	Hypothetical protein.		
GN GBS035.			
OS Streptococcus agalactiae (serotype III)			
OC Bacteria; Firmicutes; Lactobacillales; streptococci			
OC Streptococcus			
NCBI_TaxID=216495;			
[1]			
SEQUENCE FROM N.A.			
STRAIN=NEM316 / Serotype III;			
RC MEDLINE=2242508; PubMed=12354221;			
RX Glaser P., Rusniok C., Buchrieser C., Chevallier F			
RA Meadet T., Zoulli M., Couve E., Laloui L., Poyart			

Qry	1 KMNEYTVHL 9	Score 73.5%
DB	7 KLINESTIHL 15	Score 66.7%
Query Match	73.5%; Best Local Similarity 66.7%; Matches 6; Conservative 2;	Pred. No Mismatches
Qry	1 KMNEYTVHL 9	Score 73.5%
DB	7 KLINESTIHL 15	Score 66.7%; Best Local Similarity 66.7%; Matches 6; Conservative 2;
RESULT 10		
Q8DYD0	PRT;	PRELIMINARY;
ID Q8DYD0	AC Q8DYD0;	AC Q8DYD0;
DR 01-MAR-2003	DR (TREMBLrel.	DR (TREMBLrel.
DR 01-OCT-2003	DR (TREMBLrel.	DR (TREMBLrel.
DR DE	ATP-dependent protease	ATP-dependent protease
GN SMD.562.	GN SMD.562.	GN SMD.562.
OC Streptococcus mutans.	OC Firmicutes;	OC Firmicutes;
OC Streptococcaceae.	OC Lactobacillales.	OC Lactobacillales.
OC NCBI_TaxID:1309;	NCBI_TaxID:1309;	NCBI_TaxID:1309;
RN [1]	RN [1]	RN [1]
SEQUENCE FROM N.A.		
RR STRAUA159 / ATCC 700610 / Serotype	RR STRAUA159 / ATCC 700610 / Serotype	RR STRAUA159 / ATCC 700610 / Serotype
RR MEDBL=22295063; PubMed=11397186;	RR MEDBL=22295063; PubMed=11397186;	RR MEDBL=22295063; PubMed=11397186;
RA Ajdic D., McShane W.M., McLaughlin R.I.	RA Ajdic D., McShane W.M., McLaughlin R.I.	RA Ajdic D., McShane W.M., McLaughlin R.I.
RA Carson M.B., Primeaux C., Tien R., Ke Li S., Zhu H., Najjar F., Lai H., Whi	RA Carson M.B., Primeaux C., Tien R., Ke Li S., Zhu H., Najjar F., Lai H., Whi	RA Carson M.B., Primeaux C., Tien R., Ke Li S., Zhu H., Najjar F., Lai H., Whi
RA "Genome sequence of Streptococcus mutans pathogen.",	RA "Genome sequence of Streptococcus mutans pathogen.",	RA "Genome sequence of Streptococcus mutans pathogen.",
RT Proc. Natl. Acad. Sci. U.S.A. 99:1144	RT Proc. Natl. Acad. Sci. U.S.A. 99:1144	RT Proc. Natl. Acad. Sci. U.S.A. 99:1144
RT EMBL: AE014901; PAN58303.1; -	RT EMBL: AE014901; PAN58303.1; -	RT EMBL: AE014901; PAN58303.1; -
DR GO: GO-0000524; P:ATP binding; IBA.	DR GO: GO-0000524; P:ATP binding; IBA.	DR GO: GO-0000524; P:ATP binding; IBA.
DR GO: GO-0003677; P:DNA binding; IBA.	DR GO: GO-0003677; P:DNA binding; IBA.	DR GO: GO-0003677; P:DNA binding; IBA.
DR GO: GO-0004518; P:nuclelease activity;	DR GO: GO-0004518; P:nuclelease activity;	DR GO: GO-0004518; P:nuclelease activity;
DR GO: GO-0000156; P: nucleotide binding	DR GO: GO-0000156; P: nucleotide binding	DR GO: GO-0000156; P: nucleotide binding
DR GO: GO-008235; P: peptidase activity	DR GO: GO-008235; P: peptidase activity	DR GO: GO-008235; P: peptidase activity
DR GO: GO-0006849; P:nucleotide-excision	DR GO: GO-0006849; P:nucleotide-excision	DR GO: GO-0006849; P:nucleotide-excision
DR InterPro: IPR003949; AAA-ATPase.	DR InterPro: IPR003949; AAA-ATPase.	DR InterPro: IPR003949; AAA-ATPase.
DR InterPro: IPR001270; Chaperin_cTPA/B	DR InterPro: IPR001270; Chaperin_cTPA/B	DR InterPro: IPR001270; Chaperin_cTPA/B
DR Protease; Complete protease.	DR Protease; Complete protease.	DR Protease; Complete protease.
DR SEQUENCE 753 AA; EF02A2.	DR SEQUENCE 753 AA; EF02A2.	DR SEQUENCE 753 AA; EF02A2.
DR Pfam: PF00004; AAA; 2.	DR Pfam: PF00004; AAA; 2.	DR Pfam: PF00004; AAA; 2.
DR PFAM: PF02151; UTR; 1.	DR PFAM: PF02151; UTR; 1.	DR PFAM: PF02151; UTR; 1.
DR SMART: SM00382; AAA; 2.	DR SMART: SM00382; AAA; 2.	DR SMART: SM00382; AAA; 2.
DR PROSITE; PS00870; CLPAB; 1; 1.	DR PROSITE; PS00870; CLPAB; 1; 1.	DR PROSITE; PS00870; CLPAB; 1; 1.
DR PROSITE; PS05151; UTR; 1.	DR PROSITE; PS05151; UTR; 1.	DR PROSITE; PS05151; UTR; 1.
KW Mismatches	Mismatches	Mismatches
SQ	7 KLNBTATHL 15	7 KLNBTATHL 15
Query Match		
Best Local Similarity	66.7%	Score 3
Matches	6; Conservative	2; Mismatches

RESULT 11		DR Pfam; PF00271; helicase_C; 1.
ID O19815	PRELIMINARY;	PRT; 1829 AA.
AC Q19815;		
DT 01-NOV-1996	(TREMBREL 01, Created)	
DT 01-NOV-1998	(TREMBREL 08, Last sequence update)	
DT 01-OCT-2003	(TREMBREL 25, Last annotation update)	
DE F26F12.7	Protein (LET-418).	
GN F26F12.7 OR LET-418.		
OS Caenorhabditis elegans.		
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea; Rhabditida; Caenorhabditis.		
OC Rhabditidae; Pelodrinae; Nematidae; Caenorhabditis.		
NCBI_TaxID=6239;		
RN [1]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC STRAIN=BRISTOL N2;		
RX MEDLINE=94150718; PubMed=7906398;		
RA Wilson R., Ainscough R., Anddderson K., Baynes C., Berks M., Coulson A., Burton J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw N., Kirchner J., Laird N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Riffken L., Roopra A., Saunders D., Showkeen R., Smalton N., Smith A., Sonnhamer E., Stader R., Sulston J., Thierry-Mieg J., Thomas K., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sprat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."; Nature 368:32-38(1994).		
RT Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.		
RN [2]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC STRAIN=BRISTOL N2;		
RA Wilson R., Bentley D., Gartung S.; "The sequence of C. elegans cosmid F26E12.7"; Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.		
RN [3]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC STRAIN=BRISTOL N2;		
RA Waterston R.; "The sequence of C. elegans Mi-2 chromatin-remodeling proteins function in vulval cell fate determination."; Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
RN [4]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC STRAIN=BRISTOL N2;		
RA Waterston R.; "The sequence of C. elegans Mi-2 chromatin-remodeling proteins function in vulval cell fate determination."; Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
RN [5]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RA von Zelawsky T., Palladino P., Brunschwig K., Hainal A., Mueller F.; "The C. elegans Mi-2 chromatin-remodeling proteins function in vulval cell fate determination."; Development 0:0-0(2000); DR GO:GO:000785; C:chromatin; IEA.		
RL DR EMBL; U5373; ARCB; AAC25894.1; -.		
DR PIR; T34239; T34239.		
DR WormPep; F26F12.7; CE17716.		
DR GO:GO:000534; C:nucleus; IEA.		
DR GO; GO:000534; GO:000524; P:ATP binding; IEA.		
DR GO; GO:000826; P:ATP dependent helicase activity; IEA.		
DR GO; GO:003682; P:chromatin binding; IEA.		
DR GO; GO:0016787; P:hydrolyase activity; IEA.		
DR GO; GO:006333; P:chromatin assembly/disassembly; IEA.		
DR GO; GO:000655; P:regulation of transcription, DNA-dependent; IEA.		
DR InterPro; IPR000053; Chromo.		
DR InterPro; IPR001410; DEAD.		
DR InterPro; IPR002464; DEAH_box.		
DR InterPro; IPR001650; Helicase_C.		
DR InterPro; IPR000330; SNF2_N.		
DR InterPro; IPR001365; Znf_PBD.		
DR InterPro; IPR001845; chromo; 1.		
DR Pfam; PF00385; chromo; 1.		
Query Match 73.5%; Score 36; DB 5; Length 1829; Best Local Similarity 71.4%; Pred. No. 2.5e-02; Mismatches 0; Indels 0; Gaps 0;		
Qy 2 MNNEYTVH 8		
Db 765 LINETYTH 771		
RESULT 12		
Q810Y2 PRELIMINARY; PRT; 47 AA.		
ID Q810Y2		
AC Q810Y2;	(TRIMBLrel. 24, Created)	
DR 01-JUN-2003 (TRIMBLrel. 24, Last sequence update)		
DR 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)		
GN Mus spicilegus (Steppe mouse)		
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthearia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC Monroy-Burgos J.I., Bourrot P., Galtier N.; RA Monroy-Burgos J.I., Bourrot P., Galtier N.; RT Recombination explains isochores in mammalian genomes."		
RN [1]		
RL SEQUENCE FROM N.A.		
RC STRAIN=ZRU;		
RC MEDLINE=22503854; PubMed=12615004;		
RC RA Monroy-Burgos J.I., Bourrot P., Galtier N.; RT Trends Genet. 19:1228-130 (2003).		
RC EMBL; AX181235; AAOT02138; FT NON_TER		
RC DR InterPro; IPR008957; FN_III-like.		
RC FT NON_TER		
RC PT 47		
RC SEQUENCE 47 AA; 5261 MW; RT FXY (Fragment).		
RC Q802B4 PRELIMINARY; PRT; 47 AA.		
ID Q802B4		
AC Q802B4;	(TRIMBLrel. 24, Created)	
DR 01-JUN-2003 (TRIMBLrel. 24, Last sequence update)		
DR 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)		
DR FXY (Fragment).		
DR CS Mus platythrix (Flat-haired mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthearia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC NCBT TAXID=10101;		
RC SEQUENCE FROM N.A.		
RC Q802B4 PRELIMINARY; PRT; 47 AA.		
ID Q802B4		
AC Q802B4;	(TRIMBLrel. 24, Created)	
DR 01-JUN-2003 (TRIMBLrel. 24, Last sequence update)		
DR 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)		
DR FXY (Fragment).		
DR CS Mus platythrix (Flat-haired mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthearia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC NCBT TAXID=10101;		
RC SEQUENCE FROM N.A.		

RESULT 14

Q80ZB3	SEQUENCE FROM N.A.
ID Q80ZB3	PRELIMINARY;
AC Q80ZB3;	PRT; 47 AA.
DT 01-JUN-2003 (TRMBLrel. 24, Created)	
DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)	
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)	
DE FXY protein (Fragment).	
GN FXY.	
OS Arvicola terrestris (European water vole).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Arvicolinae;	
OC NCBI_TAXID=1050;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=22503854; PubMed=12615004;	
RA Montoya-Burgos J.I., Bouriot P., Galtier N.; "Recombination explains isochores in mammalian genomes.";	
RT Trends Genet. 19:128-130 (2003).	
RL EMBL; AY181232; AA062983.1; FN_III-like.	
DR InterPro; IPR008957; FN_III-like.	
FT NON-TER 1	
FT NON-TER 47	
SQ SEQUENCE 47 AA; 5261 MW; 9DC0A9F99DBCC1A6 CRC64;	
Query Match 71.4%; Score 35; DB 11; Length 47;	
Best Local Similarity 75.0%; Pred. No. 10;	
Matches 6; Conservative 0; Mismatches 2; Indels 0;	
Qy 1 KNEYTH 8	
Db 9 KQHYTVH 16	

Search completed: March 1, 2004, 17:34:39
Job time : 32.3333 secs

RESULT 15

Q80ZB0	SEQUENCE FROM N.A.
ID Q80ZB0	PRELIMINARY;
AC Q80ZB0;	PRT; 47 AA.
DT 01-JUN-2003 (TRMBLrel. 24, Created)	
DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)	
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)	
DE FXY protein (Fragment).	
GN FXY.	
OS Mastomys huberti.	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
OC NCBI_TAXID=121569;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=22503854; PubMed=12615004;	
RA Montoya-Burgos J.I., Bouriot P., Galtier N.; "Recombination explains isochores in mammalian genomes.";	
RT Trends Genet. 19:128-130 (2003).	

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OM Protein - Protein search, using sw model

Run on: March 1, 2004, 17:21:46 ; Search time 11.8889 Seconds

(without alignments)
39.081 Million cell updates/sec

Title: US-09-905-083-32

Perfect score: 40

Sequence: 1 RLISSMVKV 9

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched:

389414 seqs, 51623971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/picodata/2/iaa/5A_COMBO.pep *
2: /cgn2_6/picodata/2/iaa/5B_COMBO.pep *
3: /cgn2_6/picodata/2/iaa/6A_COMBO.pep *
4: /cgn2_6/picodata/2/iaa/6B_COMBO.pep *
5: /cgn2_6/picodata/2/iaa/PECTUS_COMBO.pep *
6: /cgn2_6/picodata/2/iaa/backfile1.sep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4	100.0	9	3	US-09-502-600-32	Sequence 32, Appl
2	40	100.0	9	4	US-09-518-23-32	Sequence 32, Appl
3	40	100.0	144	4	US-09-518-23-32	Sequence 4, Appl
4	40	100.0	154	3	US-09-561-416-7	Sequence 7, Appl
5	40	100.0	161	3	US-09-561-416-8	Sequence 8, Appl
6	40	100.0	224	3	US-08-944-48-33	Sequence 33, Appl
7	40	100.0	225	2	US-08-955-114-12	Sequence 12, Appl
8	40	100.0	225	2	US-09-037-337-4	Sequence 4, Appl
9	40	100.0	225	2	US-09-154-344-12	Sequence 12, Appl
10	40	100.0	225	4	US-09-644-600-4	Sequence 4, Appl
11	40	100.0	225	4	US-19-654-60A-4	Sequence 3, Appl
12	40	100.0	253	2	US-08-557-146-2	Sequence 2, Appl
13	40	100.0	253	2	US-08-824-87-3	Sequence 3, Appl
14	40	100.0	253	2	US-09-134-344-2	Sequence 2, Appl
15	40	100.0	253	3	US-08-930-188-2	Sequence 2, Appl
16	40	100.0	253	3	US-09-210-084-2	Sequence 3, Appl
17	40	100.0	253	4	US-09-764-762-3	Sequence 2, Appl
18	40	100.0	253	5	PCT-US96-04224-2	Sequence 110, Appl
19	36	90.0	9	3	US-09-502-600-110	Sequence 110, Appl
20	36	90.0	9	4	US-09-918-243-110	Sequence 79, Appl
21	31	77.5	9	3	US-09-50-600-79	Sequence 87, Appl
22	31	77.5	9	3	US-09-501-600-87	Sequence 79, Appl
23	31	77.5	9	4	US-09-918-243-79	Sequence 87, Appl
24	31	77.5	9	4	US-09-918-243-87	Sequence 7506, Appl
25	29	75.0	156	4	US-09-352-7506	Sequence 15, Appl
26	29	72.5	571	4	US-09-690-942-15	Sequence 2, Appl
27	29	72.5	582	1	US-08-261-086-2	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-092-600-32
; Sequence 32, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
; TITLE OF INVENTION:
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09-502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS.: 136
; SEQ ID NO. 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-512-600-32

RESULT 2
US-09-918-243-32
; Sequence 32, Application US/09918243
; Patent No. 6274403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT FILING DATE: 2001-07-30
; CURRENT APPLICATION NUMBER: US/09-918,243
; PRIOR APPLICATION NUMBER: US/09-764-762-3
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS.: 136
; SEQ ID NO. 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE:
 ; NAME/KEY: CHAIN
 ; OTHER INFORMATION: Residues 123-131 of the SCCE protein
 US-09-918-243-32

Query Match Similarity 100.0%; Score 40; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLISSMVKV 9
 Db 1 RLISSMVKV 9

RESULT 3
 US-09-618-259-4
 Sequence 4, Application US/09618259
 Patent No. 6642013
 GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; ATTORNEY: Underwood, Lowell J.
 ; TITLE OF INVENTION: A No. 6291663el Transmembrane Serine Protease
 ; FILE REFERENCE: D61.92
 ; CURRENT APPLICATION NUMBER: US/09/261,416A
 ; CURRENT FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO: 8

Length: 161
 TYPE: PRT
 ORGANISM: Unknown

FEATURE:
 ; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
 ; FILE REFERENCE: D6020CIP2
 ; CURRENT APPLICATION NUMBER: US/09/618,259
 ; CURRENT FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: US 09/127,444
 ; PRIOR FILING DATE: 1998-08-21
 ; SEQ ID NO: 4
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: unknown

NAME/KEY: DOMAIN
 OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
 OTHER INFORMATION: enzyme (scce) catalytic domain

US-09-618-259-4

Query Match Similarity 100.0%; Score 40; DB 4; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLISSMVKV 9
 Db 60 RLISSMVKV 68

RESULT 4
 US-09-261-416-7
 Sequence 7, Application US/09261416A
 Patent No. 6291663
 GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; ATTORNEY: Underwood, Lowell J.
 ; TITLE OF INVENTION: A No. 6291663el Transmembrane Serine Protease
 ; FILE REFERENCE: D61.92
 ; CURRENT APPLICATION NUMBER: US/09/261,416A
 ; CURRENT FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO: 7
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Unknown

FEATURE:
 ; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
 ; OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
 ; OTHER INFORMATION: domain in TADG-12

Query Match Similarity 100.0%; Score 40; DB 3; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0.77;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLISSMVKV 9
 Db 69 RLISSMVKV 77

RESULT 5
 US-09-261-416-8
 Sequence 8, Application US/09261416A
 Patent No. 6291663
 GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; ATTORNEY: Underwood, Lowell J.
 ; TITLE OF INVENTION: A No. 6291663el Transmembrane Serine Protease
 ; FILE REFERENCE: D61.92
 ; CURRENT APPLICATION NUMBER: US/09/261,416A
 ; CURRENT FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO: 8

Length: 161
 TYPE: PRT
 ORGANISM: Unknown

FEATURE:
 ; OTHER INFORMATION: Serine protease catalytic domain of hepsin (Heps)
 ; OTHER INFORMATION: homologous to similar domain in TADG-12

US-09-261-416-8

Query Match Similarity 100.0%; Score 40; DB 3; Length 161;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLISSMVKV 9
 Db 75 RLISSMVKV 83

RESULT 6
 US-08-944-483-33
 Sequence 33, Application US/08944483
 Patent No. 6233456
 GENERAL INFORMATION:
 ; APPLICANT: COHEN, MAURICE
 ; ATTORNEY: COLPITTS, TRACEY L.
 ; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
 ; NUMBER OF SEQUENCES: 76
 ; ADDRESS: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/944,483
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Chery L.
 REGISTRATION NUMBER: 35,441
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEX: 95 RLSSMVKV 103

SEQUENCE CHARACTERISTICS:
 LENGTH: 224 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6232456e

US-08-944-483-33

Query Match. Score 40; DB 3; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 RLSSMVKV 9
 Db 94 RLSSMVKV 102

RESULT 7
 US-08-557-146-12
 Sequence 12, Application US/08557146
 Patent No. 5834230

GENERAL INFORMATION:
 APPLICANT: Egelrud, Torbjorn
 APPLICANT: Hansson, Lennart
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case, Patent Department
 STREET: 1115 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-7787

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION NUMBER: US/08/557,146
 APPLICATION NUMBER: US/08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113

SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: polypeptide

US-08-557-146-12

Query Match. Score 40; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 RLSSMVKV 9

Db 95 RLSSMVKV 103

RESULT 8
 US-09-027-337-4
 Sequence 4, Application US/09027337B
 Patent No. 5972616

GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Tanimoto, Hirotoshi
 TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in Breast and Ovarian Carcinomas

FILE REFERENCE: D6064
 CURRENT APPLICATION NUMBER: US/09/027,337B
 CURRENT FILING DATE: 1998-02-20
 NUMBER OF SEQ ID NOS: 13

SEQ ID NO. 4
 LENGTH: 225

Query Match. Score 40; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;

QY 1 RLSSMVKV 9
 Db 95 RLSSMVKV 103

OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to similar domain in TADG-15

US-09-027-337-4

Query Match. Score 40; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;

QY 1 RLSSMVKV 9
 Db 95 RLSSMVKV 103

OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to similar domain in TADG-15

US-09-027-337-4

RESULT 9
 US-09-154-344-12
 Sequence 12, Application US/09154344
 Patent No. 5981256

GENERAL INFORMATION:
 APPLICANT: Egelrud, Torbjorn
 APPLICANT: Hansson, Lennart
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case, Patent Department
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2787

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION NUMBER: US/08/557,146
 APPLICATION NUMBER: US/08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113

SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: polypeptide

US-08-557-146-12

Query Match. Score 40; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;

QY 1 RLSSMVKV 9

SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acids
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: polypeptide

US-09-154-344-12

Query Match Score 100.0%; Pred. No. 1.1; Length 225;
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 95 RLSSMVKV 103

RESULT 12

US-08-557-146-2

; Sequence 2, Application US/08557146
 ; Patent No. 584290

OTHER INFORMATION: SCCE

US-09-654-600A-4

Query Match Score 100.0%; Pred. No. 1.1; Length 225;
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 95 RLSSMVKV 103

RESULT 10

US-09-644-600-4

Sequence 4, Application US/09644600

PATENT NO. 651500

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

FILE REFERENCE: D6064CIP/D

CURRENT FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: 09/027,337

PRIOR FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 4

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: SCCE

US-09-644-600-4

Query Match Score 100.0%; Pred. No. 1.1; Length 225;
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 95 RLSSMVKV 103

RESULT 11

US-09-654-600A-4

Sequence 4, Application US/09654600A

PATENT NO. 6639741

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

FILE REFERENCE: D6064CIP/D

CURRENT FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 98

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-654-600A-4

Query Match Score 100.0%; Pred. No. 1.1; Length 225;
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 95 RLSSMVKV 103

RESULT 13

US-08-824-874-3

; Sequence 3, Application US/08824874
 ; Patent No. 5953300

OTHER INFORMATION:

APPLICANT: Lal, Preeti

FILE REFERENCE: D6064CIP/D

CURRENT FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 09/027,337

PRIOR FILING DATE: 1998-02-20

LENGTH: 225

NUMBER OF SEQ ID NOS: 98

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-08-824-874-3

Query Match Score 100.0%; Pred. No. 1.2; Length 253;
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

RESULT 14

US-08-824-874-4

; Sequence 4, Application US/08824874
 ; Patent No. 5953300

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

FILE REFERENCE: D6064CIP/D

CURRENT FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 98

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-08-824-874-4

Query Match Score 100.0%; Pred. No. 1.2; Length 253;
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKV 9
 Db 123 RLSSMVKV 131

STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/324,874
 FILING DATE: Filed Herewith
 CLASSIFICATION: 51.4
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0252 US
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 532504

US-08-874-3

Query Match Score 40; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.2%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKRV 9
 Db 123 RLSSMVKRV 131

RESULT 14
 US-09-154-344-2
 Sequence 2, Application US/09154344
 / Patent No. 5982256
 / GENERAL INFORMATION:
 / APPLICANT: Egeland, Torbjorn
 / TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 / NUMBER OF SEQUENCES: 17
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: White & Case, Patent Department
 / STREET: 1155 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: U.S.A.
 / ZIP: 10036-2787

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/154,344
 FILING DATE: 16-SEP-1998
 CLASSIFICATION:
 APPLICATION NUMBER: US 08/557,146
 FILING DATE: 14-DEC-1995

Query Match Score 40; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.2%;

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sterner, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEX/FAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-09-154-344-2

Query Match Score 40; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.2%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKRV 9
 Db 123 RLSSMVKRV 131

RESULT 15
 US-08-910-188-2
 Sequence 2, Application US/08930188
 / Patent No. 6093397
 / GENERAL INFORMATION:
 / APPLICANT: Dixon, Eric P.
 / APPLICANT: Johnstone, Edward M.
 / APPLICANT: Little, Sheila P.
 / TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
 / TITLE OF INVENTION: RELATED NUCLEIC ACIDS
 / NUMBER OF SEQUENCES: 3
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Eli Lilly and Company
 / STREET: Lilly Corporate Center
 / CITY: Indianapolis
 / STATE: Indiana
 / COUNTRY: United States of America
 / ZIP: 46285

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/930,188
 FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Blalock, Donna K.
 / REGISTRATION NUMBER: 38,082
 / REFERENCE/DOCKET NUMBER: X92319
 / TELECOMMUNICATION INFORMATION:
 / APPLICATION NUMBER: US 08/416,257
 / FILING DATE: 04-APR-1995
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Blalock, Donna K.
 / REGISTRATION NUMBER: 38,082
 / REFERENCE/DOCKET NUMBER: X92319
 / TELEPHONE: 317-277-1090
 / TELEFAX: 317-276-3861
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 253 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 US-08-930-188-2

Query Match Score 40; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.2%;

	Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	RLSSMYKCV	9							
Db	123	RLSSMYKCV	131							

Search completed: March 1, 2004, 17:38:23
Job time : 12.8889 secs


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Best Local Similarity 100.0%; Pred. No. 1.e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gap 1 RLSNNYKRV 9
      ||||| |
      1 RLSNNYKRV 9

```

WPI; 2003-381626/36.
N-PSDB; ADA05743.

RESULT 2
ADA05744
D ADA05744 standard; protein; 224 AA.

MUSEUMS - MUSE

COX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOX-associated disorders, e.g. diabetes, or dyslipidemia, and in chromosome mapping, tissue typing or aetogenomics.

Claim 1; Page 172; 586PP; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX Protein of the invention described above; (5) a cell comprising the nucleic acid molecule described above; (4) a vector comprising the nucleic acid molecule described above; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) method for producing the above polypeptide. NOVX sequences have antiabietic, anorectic, antibacterial, viricide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorder, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

DD
RESULT 3
AAB98502
ID: AAB98502 standard; protein; 225 AA.
XX
AAB98502;
AC
AC
AC
XX

03-AUG-2001 (First entry)
Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
Human; TAG-15; cytostatic; vaccine; ovarian tumour; cancer;
tumour antigen-derived gene 15; serine protease;
Stratum Corneum Chymotryptic Enzyme; SCCE.
Homo sapiens.

X 26-APR-2001.
 D
 X 20-OCT-2000; 2000WO-US029095.
 X
 X 20-OCT-1999; 99US 00421213.
 X
 X (UYAR-) UNIV ARKANSAS.
 A
 X O'brien T, Tanimoto H;
 X
 X WPI; 2001 381031/4C.
 X
 X Novel extracellular serine protease, termed tumor antigen-derived Gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
 X
 X Example 10; Fig 1; 130pp, English.
 X
 X The present invention relates to human tumour antigen-derived Gene 15 (TADG-15) protein and coding sequence (see AAH21601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15 Sequence 225 AA; Score 100.0%; DB 4; Length 225;
 X
 X Query Match Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
 X
 X Matches 9; Conservative 0; Gaps 0;

RESULT 4	
ADA05742	ADA05742 standard; protein SEQ ID NO:102.
XX	ADA05742;
AC	Human NOV18 f protein SEQ ID NO:102.
XX	06-NOV-2003 (first entry)
DB	Human NOV18 f protein SEQ ID NO:102.
XX	human; NOVX; anti-diabetic; anorectic; immunomodulator; cytostatic; nootropic; antiparkinsonian; antilipemic; genotoxic; metabolic disorder; diabetes; obesity; neurodegenerative disorder; Alzheimer immune disorder; haematopoietic
XX	XX
OS	Homo sapiens.
XX	XX
PN	W02003029424-A2.
XX	XX
PD	10-APR-2003.
XX	XX
PF	02-OCT-2002; 2002WO-US031373.
XX	XX
PR	02-OCT-2001; 2001US-0326483P.
PR	05-OCT-2001; 2001US-0327431P.
PR	05-OCT-2001; 2001US-0327441P.
PR	09-OCT-2001; 2001US-0327911P.
PR	09-OCT-2001; 2001US-0328029P.
PR	09-OCT-2001; 2001US-0328044P.
PR	12-OCT-2001; 2001US-0328056P.
PR	12-OCT-2001; 2001US-0328494P.

PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0341629P.
 PR 29-OCT-2001; 2001US-0345575P.
 PR 01-NOV-2001; 2001US-0345577P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373848P.
 PR 22-APR-2002; 2002US-0374177P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381042P.
 PR 28-MAY-2002; 2002US-038356P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-039135P.
 PR 01-OCT-2002; 2002US-00263511.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Smithson G, Millet J, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Pattrurajan M, Spytek KA, Edinger SR, Ellerman K, Malvankar UM;
 PI Ort T, Gorman L, Zerhouni BD, Anderson DM, Zhong M, Catterton E;
 PI Jii W, Miller CE, Rastelli L, Stone DJ, Peña CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agree ML, Berghs C, D'Pippo VA;
 PI Eisner AJ, Ganguli EA, Rieger DK, Spaderna SK;
 XX DR 2003-381626/36.
 XX PT N-PSDB; ADR05741.
 XX PT PT PT PT PT PT
 XX PS XX
 XX The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide associated with the above mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibiotic, neuroprotective, anti-Parkinsonian
 CC immunomodulator, cytostatic, nootropic, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematochemical disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation

PI	Smithson G, Millet J, Payman JA, Kerkuda R, Ju J, Li L, Guo X;
PI	Patturajan M, Spock KA, Edinger SR, Elleman K, Malyanan UM;
PI	Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI	Ji W, Miller CE, Rastelli L, Stone DJ, Pana CBA, Shenoy SG;
PI	Shimke RS, Rothenberg ME, Leach MD, Agee ML, Bershts C, Dippio VA;
PI	Eisen AJ, Gangoli BA, Rieger DK, Spederna SK;
XX	DR: 2003-181626/36.
XX	DR N-FSDB; ADA05731.
PT	New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
PT	XX
PT	Claim 1 ; Page 169-170 ; 586pp; English.
PT	XX
XX	CC The present invention describes NOVX proteins, where X can be 1 to 55 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide CC described above and a carrier; (2) a kit comprising, in one or more CC containers, the composition described above; (3) an isolated nucleic acid CC molecule which encodes a NOVX protein of the invention; (4) a vector CC comprising the nucleic acid molecule described above; (5) a cell CC comprising the above vector; (6) an antibody that immunospecifically CC binds to the polypeptide described above; (7) methods for determining the CC presence or amount of the above polypeptide or nucleic acid molecule in a CC sample; (8) methods for determining the presence of or predisposition to CC a disease associated with altered levels of expression of the above CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a CC method of identifying an agent that binds to the polypeptide described CC above; (10) a method for identifying a potential therapeutic agent for CC use in treating a pathology that is related to an aberrant expression or CC aberrant physiological interactions of the polypeptide; (11) a method of CC screening for a modulator of activity or of latency or predisposition to CC a pathology associated with the polypeptide; (12) a method for modulating CC the activity of the polypeptide described above; (13) methods of treating CC or preventing a pathology associated with the above polypeptide in a CC mammal; and (14) a method for producing the above polypeptide. NOVX CC sequences have antidiabetic, anorectic, antibacterial, virucide, CC immunomodulator, cytotactic, neuroprotective, anti-parkinsonian CC and antilipase activities, and can be used in gene therapy. The CC polypeptide is useful in manufacturing a medicament for treating a CC syndrome associated with a human disease. The polypeptide or the nucleic CC acid molecule may be used to diagnose, treat or prevent metabolic CC disorders such as diabetes or obesity, infections, cachexia, cancer, CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's CC disease, immune disorders and hematopoietic disorders and various CC dyslipidemias. The nucleic acids can also be used as hybridisation CC probes, in chromosome mapping, tissue typing, preventive medicine and CC pharmacogenomics. The present sequence represents a human NOVX from the CC present invention.
XX	Sequence 250 AA;
SQ	Query Match 1 RLSSMVKKY 9 Best Local Similarity 100.0% ; Score 40 ; DB 6 ; Length 250 ; Matches 9 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
Qy	1 RLSSMVKKY 9
Db	120 RLSSMVKKV 128
RESULT 6	
ADA05734	
ID	ADA05734 standard; protein; 252 AA.
XX	
XX	ADA05734 ;
XX	DT 06-NOV-2003 (first entry)
XX	Human NOV18b protein SEQ ID NO:94.

GenCore version 5.1.6
 (c) 1993 - 2004 Compugen Ltd.

Copyright - protein search, using sw model

Run on: March 1, 2004, 17:16:55 ; Search time 45.556 seconds
 Perfect score: 41 ; (without alignment(s))
 Sequence: 1 MARSLLPL 9

Title: US-09-905-083-86
 Scoring table: BLUSUM62
 GappT 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04;*
 1: GeneseqP1980s;*
 2: GeneseqP1990s;*
 3: GeneseqP2000s;*
 4: GeneseqP2001s;*
 5: GeneseqP2002s;*
 6: GeneseqP2003ab;*
 7: GeneseqP2003bs;*
 8: GeneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Residue No.	Score	Query	Match Length	DB ID	Description
1	41	100.0	9	AEE08291	Aee0291 Human str
2	41	100.0	136	ABG23378	Abg23378 Novel hum
3	41	100.0	198	ADA05736	Ada05736 Human NOV
4	41	100.0	253	AIR67888	Aar67888 Human str
5	41	100.0	253	AWW05383	Aaw05383 Human amy
6	41	100.0	253	ABB84421	Abb84421 Human SCC
7	41	100.0	253	ABB84406	Abb84406 Human SCC
8	41	100.0	253	AAB182740	Aau8740 Amino aci
9	41	100.0	253	ABU07440	Abu07440 Protein d
10	41	100.0	253	ABU07471	Abu07471 Protein d
11	41	100.0	253	ABR58471	Abr58471 Human str
12	41	100.0	253	ABBB0484	Adb8484 ovarian c
13	41	100.0	257	AB21326	Aab21326 Human HSC
14	36	87.8	9	AAB08320	Aae0320 Human str
15	36	87.8	818	ABP98135	Abb98135 Human PMM
16	36	87.8	818	AAU82753	Aau82753 Amino aci
17	35	85.4	475	AB10657	Aae10657 Secreted
18	35	85.4	475	AAB02609	Aae02609 Human sec
19	35	85.4	475	ABB78618	Abb78618 Secreted
20	35	85.4	518	AAW61362	Aaw61362 Aspartic
21	35	85.4	518	AAV13799	Aay13799 Human asp
22	35	85.4	518	AAV22239	Aay22239 Human CSP
23	35	85.4	518	AAY41714	Aay41714 Human PRO
24	35	85.4	518	AAV88424	Aay88424 Human asp
25	35	85.4	518	AAB44270	Aab44270 Human PRO

Sequence 9 AA;

Query Match

100.0%; Score 41; DB 4; Length 9;

ALIGNMENTS

RESULT 1		AEE08291		AEE08291 Standard; peptide; 9 AA.	
ID	XX	ID	XX	AC	AEE08291;
	XX		XX	DT	01-NOV-2001 (first entry)
	XX		XX	DE	Human stratum corneum chymotrypsin enzyme peptide #56 (residues 1-9).
	XX		XX	XX	Stratum corneum chymotrypsin enzyme; SCCE; cytosstatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; anticancer therapy; malignant hyperplasia.
	XX		OS	OS	Homo sapiens.
	XX		XX	PN	WO20010159158-A1.
	XX		XX	PD	16-AUG-2001.
	XX		XX	PF	07-FEB-2001; 2001WO-US003977.
	XX		XX	PR	11-FEB-2000; 2000US-00502600.
	XX		XX	XX	(UTAR-) UNIV ARKANSAS.
	XX		XX	PI	O'Brien TJ;
	XX		XX	XX	DR WPI; 2001-51467/56.
	XX		XX	PT	Diagnosing cancer comprises detecting stratum corneum chymotrypsin peptide.
	XX		XX	PS	Claim 25; Page 114; 127pp; English.
	XX		XX	CC	The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis and therefore, markers indicative of their presence or absence are useful for the diagnosis of Cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE Oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
	XX		XX	CC	Sequence 9 AA;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 MARSLLPL 9
 DB 1 MARSLLPL 9

RESULT 2
 ABG23378

ID ABG23378 standard; protein; 136 AA.
 XX

AC AC05736;
 XX

DT 18-FEB-2002 (first entry)
 XX

DE Novel human diagnostic protein #23369.
 XX

XX Human; chromosome mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.
 XX

PN WO200125067-A2.
 XX

PD 11-OCT-2001.
 XX

PF 30-MAR-2001; 2001WO-US008631.
 XX

PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.
 XX

PI Dumanac RT, Liu C, Tang YT;
 XX

DR 2001-633962/73.
 DR N-PSDB; AAS87565.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20: SEQ ID NO 533737; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (III). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful to treat disease states involving (III), normal activity of (III) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations, and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG1037 represent novel human diagnostic sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX Sequence 136 AA;

CC Query Match 100.0%; Score 41; DB 4; Length 136;
 CC Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLPL 9
 DB 7 MARSLLPL 15

RESULT 3
 ADA05736

ID ADA05736 standard; protein; 198 AA.
 XX

AC ADA05736;
 XX

DT 06-NOV-2003 (first entry)
 XX

DE Human NOV18c protein SEQ ID NO:96.
 XX

XX human; NOV18c; antidiabetic; anorectic; antibacterial; virucide;

XX immunomodulator; cytostatic; nootropic; neuroprotective;

XX anti-parkinsonian; antilipamic; gene therapy; human disease;

XX metabolic disorder; diabetes; obesity; infection; cachexia; cancer;

XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

XX immune disorder; haematopoietic disorder; dyslipidaemia.

XX Homo sapiens.
 OS

PN WO2003029424-A2.
 XX

PD 10-APR-2003.
 XX

PF 02-OCT-2002; 2002WO-US031373.
 XX

PR 02-OCT-2001; 2001US-0356483P;
 PR 05-OCT-2001; 2001US-037435P;
 PR 05-OCT-2001; 2001US-037449P;
 PR 09-OCT-2001; 2001US-0327917P;
 PR 09-OCT-2001; 2001US-0328029P;
 PR 09-OCT-2001; 2001US-0328044P;
 PR 09-OCT-2001; 2001US-0328056P;
 PR 12-OCT-2001; 2001US-0328849P;
 PR 15-OCT-2001; 2001US-0329414P;
 PR 17-OCT-2001; 2001US-0330142P;
 PR 18-OCT-2001; 2001US-0330309P;
 PR 22-OCT-2001; 2001US-0341058P;
 PR 24-OCT-2001; 2001US-0339266P;
 PR 24-OCT-2001; 2001US-0333629P;
 PR 29-OCT-2001; 2001US-0334975P;
 PR 01-NOV-2001; 2001US-0343635P;
 PR 17-APR-2002; 2002US-0373260P;
 PR 19-APR-2002; 2002US-0373815P;
 PR 19-APR-2002; 2002US-0373821P;
 PR 19-APR-2002; 2002US-0373826P;
 PR 22-APR-2002; 2002US-0373884P;
 PR 22-APR-2002; 2002US-0374977P;
 PR 16-MAY-2002; 2002US-0381031P;
 PR 2002US-0381038P;
 PR 16-MAY-2002; 2002US-0381042P;
 PR 17-MAY-2002; 2002US-03816422P;
 PR 28-MAY-2002; 2002US-038356P;
 PR 29-MAY-2002; 2002US-038383P;
 PR 25-JUN-2002; 2002US-038335P;
 PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

CC PI Sattarjan M, Spyrek KA, Billerman SR, Billerman K, Malaysian UM;

CC PI Ort T, Gorman L, Zethusen BD, Anderson DW, Zhong M, Catterton E;

CC PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;

CC PI Shimkets RA, Rothenberg ME, Leach MD, Agree ML, Bergs C, Dipippo VA;

CC PI Eisner AJ, Ganguli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

DR N-PSDB; ADA05735.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

PT PT

PT PT

PT PT

XX XX

PS Claim 1; Page 170; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have anti-diabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, neuroprotective, antiparkinsonian and anti-lipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

XX Sequence 198 AA;

Query Match Score 41; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
Dd 1 MARSLLPL 9

Query Match Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
Dd 1 MARSLLPL 9

RESULT 4
AAR67888 ID AAR67888 standard; protein; 253 AA.
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 01-AUG-1995 (first entry)
XX DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
XX KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX OS Homo sapiens.
XX PN WO950061-A1.

RESULT 4
AAR67888 ID AAR67888 standard; protein; 253 AA.
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 01-AUG-1995 (first entry)
XX DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
XX KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX OS Homo sapiens.
XX PN WO950061-A1.
XX PD 05-JAN-1995.

XX 20-JUN-1994; 94WO-IB000166.
PF XX
PR 18-JUN-1993; 93DK-00000725.
PA (SYMB-) SYMBICOM AB.
XX
PI Egeland T, Hansson L;
XX WPI: 1995-052088/07.
DR N-PSDB; AAQ81203.
XX Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and PR related vectors, transformed cells and polypeptides, useful for treating PT skin disorders, e.g. acne or psoriasis, and for identification of PT specific inhibitors.
XX Disclosure; Page 97; 137pp; English.
XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic CC and skin care products, especially to treat and prevent acne, xerosis, CC or other hyperkeratotic conditions (e.g. callousities or keratosis CC recombinantly following mammal, insect, plant, or microorganism CC transformation with plasmid PS507. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 253 AA;
Query Match Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARSLLPL 9
Dd 1 MARSLLPL 9

RESULT 5
ID AAV05383
AAV05383 standard; protein; 253 AA.
AC AAV05383;
XX AC
XX DT 31-DEC-1996 (first entry)
XX DE Human amyloid precursor protein protease.
XX DE Human amyloid precursor protein protease; Alzheimer's disease; diagnosis; KW therapy.
XX OS Homo sapiens.
XX PN WO931112-A1.
XX PR 04-APR-1995;
XX PD 10-OCT-1996.
XX PA (ELLI) LILLY & CO ELI.
XX PF 02-APR-1996;
XX PR 04-APR-1995;
XX DR N-PSDB; AAQ3983.
XX PT New isolated human amyloid precursor protein protease - used to develop PT products for the treatment or diagnosis of associated conditions, esp. PT Alzheimer's disease.
XX
Claim 1; Page 44-45; 55pp; English.
PS

XX Human amyloid precursor protein protease (AAW053B3) is involved in the CC processing or clearance of amyloid precursor protein to form beta-amyloid CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAI39783) CC obtained from a human lung library. Recombinant protease can be produced in CC transformed or human host cells. It is used to develop products for the design CC and testing of caps. useful for treating or preventing conditions CC associated with beta-amyloid peptide, esp. Alzheimer's disease
 XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 2; Length 253;
 Best Local Similarity 100.0%; Prcd. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARSLLPLP 9
 Db 1 MARSLLPLP 9

RESULT 6
 ABB84421 ID ABB84421 standard peptide; 253 AA.
 XX AC ABB84421;

XX 08-NOV-2002. (first entry)

XX Human SCCE protein N-terminal fragment SEQ ID 48.

KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
 KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
 KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
 KW pruritus; atopic dermatitis; epidermal; acne; itch; KLK7; enzyme.
 OS Homo sapiens.

XX WO20020262135-A2.

XX PD 15-AUG-2002.

XX PP 08-FEB-2002; 2002WO-IB001360.

XX PR 09-FEB-2001; 2001CA-02332655.

XX PR 09-FEB-2001; 2001DK-00000218.

XX PA (EGEL/) EGELRUD T.
 PA (HANS/) HANSSON L.

XX PI Egelrud T, Hansson L;

XX DR WPI, 2002-643380/69.

PT Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 XX Example 6; Page 37; 74pp; English.

CC This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide sequence
 CC comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous scce
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathogenic condition, for development or testing of a
 CC cosmetic or pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC diagnostic method. It can also be used as a model for a skin disease or

XX compound or composition effective for the prevention or treatment of
 CC inflammatory skin diseases selected from diseases consisting of epidermal
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful
 CC as a model for further studies of itch mechanisms and the testing of
 CC potential compounds and compositions for relieve of various skin diseases
 CC where itch is a component. This sequence represents the N-terminal
 CC fragment of the human stratum corneum chymotryptic enzyme, SCCE
 CC synonymous with human kallikrein 7 (KLK7), used in the development of the
 CC transgenic mammals described in the invention
 XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 5; Length 253;
 Best Local Similarity 100.0%; Prod. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARSLLPLP 9
 Db 1 MARSLLPLP 9

RESULT 7
 ABB84406 ID ABB84406 standard; protein; 253 AA.

XX AC ABB84406;

XX DT 08-NOV-2002 (first entry)

XX DE Human SCCE protein.

XX KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;

XX KW serine protease; transgenic mammal; skin; skin disease; skin cancer;

XX KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;

XX KW pruritus; atopic dermatitis; epidermal; acne; itch; KLK7; enzyme.

OS Homo sapiens.
 XX PN WO20020262135-A2.
 XX PD 15-AUG-2002.
 XX PP 08-FEB-2002; 2002WO-IB001300.
 XX PR 09-FEB-2001; 2001CA-02332655.
 XX PR 09-FEB-2001; 2001DK-00000218.
 XX PA (EGEL/) EGELRUD T.
 PA (HANS/) HANSSON L.
 XX PI Egelrud T, Hansson L;
 XX DR WPI, 2002-643380/69.
 PT Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 XX Example 6; Page 37; 74pp; English.

CC This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide sequence
 CC comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous scce
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathogenic condition, for development or testing of a
 CC cosmetic or pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC diagnostic method. It can also be used as a model for a skin disease or

XX Claim 10; Page 58-59; 74pp; English.

XX DR N-PSSD; ABQ76226.

XX Transgenic mammal or its embryo useful as model for stratum corneum chymotryptic
 PT PT enzyme operably linked to promoter that drives its expression in skin.
 XX PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT PT enzyme operably linked to promoter that drives its expression in skin.
 XX PT WPI, 2002-643380/69.
 XX DR N-PSSD; ABQ76226.

skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from the diseases consisting of epidermal hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritis, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions of itch mechanisms and the testing of where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous with human kallikrein 7 (KuR7) and is used in the development of the transgenic mammals described in the invention.

Sequence 253 AA;

```
Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
Qy 1 MARSLLPL 9
          ||||| |
          1 MARSLLPL 9
Db. 1 MARSLLPL 9
```

Sequence 253 AA;

```
RESULT 8
AAU82740 standard; protein; 253 AA.
ID AAU82740
XX DT 23-APR-2002 (first entry)
AC AAU82740;
XX DE Amino acid sequence of novel human protease #39.
XX KW Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychologic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
XX OS Homo sapiens.
XX PN WO200200860-A2.
XX PD 03-JAN-2002.
XX PR 26-JUN-2001; 2001WO-US020171.
XX PR 26-JUN-2000; 2000US-0214047P.
XX PA (SUGEN INC.
XX PI Ploynomial G., Whyte D., Sudarsanam S., Manning G., Caenepel S., Charydzak G.; ABK31782.
XX DR WPI; 2002-139913/18.
XX DR N-PSDB; ABK31782.
```

Claim 6:

PT FIG 2N; 313PP; English.

CC Nucleic acids encoding novel human proteases, useful for treating diseases and disorders such as cancer, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders.

XX FS

CC The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and

coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rheumatoid arthritis and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypertension, hypotension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease), and dyskinetias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention.

XX SQ Sequence 253 AA;

```
Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
Qy 1 MARSLLPL 9
          ||||| |
          1 MARSLLPL 9
Db. 1 MARSLLPL 9
```

XX RESULT 9
AB007440

```
ID AB007440 standard; protein; 253 AA.
XX AC AB007440;
XX DT 28-JAN-2003 (first entry)
AC XX DE Protein differentially regulated in prostate cancer #43.
XX KW Prostate cancer; gene expression; differential regulation;
molecular marker; drug target; cancer detection; cancer diagnosis;
cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX KW XX OS Homo sapiens.
XX PN WO200281638-A2.
XX PD 17-OCT-2002.
XX PR 08-APR-2002; 2002WO-US010824.
XX PR 06-APR-2001; 2001US-0281731P.
XX PR 06-APR-2001; 2001US-0281732P.
```

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.

XX PI Sun Z., Jay G.;

XX DR WPI; 2003-058520/05.

XX DR N-PSDB; ABX10343.

XX PT Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue and assessing therapeutic or preventive intervention in prostate cancer patients.

XX PS Claim 1; Page 293-294; 4-6PP; English.

CC The invention describes Genes (I) which are differentially regulated in prostate cancer. (I) is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer

cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, staging, grading, assessing, monitoring, prognosticating, preventing, or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide. (I) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer

Sequence 253 AA;

Query Match Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARSLLPL 9
Db 1 MARSLLPL 9

RESULT 10

ABU07471 standard, protein, 253 AA.

ABU07471;

28-JAN-2003 (First entry)

Protein differentially regulated in prostate cancer #74.
XX Prostate cancer; gene expression; differential regulation;
XX molecular marker; drug target; cancer detection; cancer diagnosis;
XX cancer staging; cancer grading; cancer assessing; cancer monitoring.
OS Homo sapiens.

PN WO200291638-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-US010824.

PR 06-APR-2001; 2001US-0281731P.

PR 06-APR-2001; 2001US-0281733P.

PA (ORIG-) ORIGENE TECHNOLOGIES INC.

PI Sun Z, Jay G;

XX WPI; 2003-058520/05.

DR N-PADB; ABX10375.

XX Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
PT Claim 1; Page 351; 416pp; English.
XX The invention describes genes (I) which are differentially regulated in

prostate cancer. (I) is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the polypeptide, and the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, grading, assessing, monitoring, prognosticating, preventing, or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide. (I) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer

Sequence 253 AA;

Query Match Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
Db 1 MARSLLPL 9

RESULT 11

ABR58471

ID ABR58471

AC ABR58471;
XX DT 07-JUL-2003 (First entry)
XX DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone 01676P.
XX KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX OS Homo sapiens.
XX PN WO2003029468-A1.
XX PD 10-APR-2003.
XX PR 02-OCT-2002; 2002WO-US031467.
XX PR 02-OCT-2001; 2001US-0322135P.
XX PR 30-MAY-2002; 2002US-0384531P.
XX PA (CORY) CORYXA CORP.
XX PI Algate PA, Mannion J;
XX DR WPI; 2003-372001/35.

XX New polynucleotide and polypeptide useful for diagnosing and/or treating
 PT cancer, particularly ovarian cancer, and as a vaccine.
 XX Claim 2; Page 157-158; 169pp; English.

CC The invention relates to a novel isolated polynucleotide. The
 CC polynucleotides of the invention have cytostatic activity, and may have a
 CC use in gene therapy, and in a vaccine. The composition and methods are
 CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
 CC The composition may also be used as a vaccine to prevent cancer. The
 CC present sequence is used in the exemplification of the invention.
 XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLPLP 9
 Db 1 MARSLLPLP 9

RESULT 12
 ADB80484 standard; protein; 253 AA.
 XX ADBB0484;
 AC ADBB0484;
 XX DT 04-DEC-2003 (first entry)
 XX Ovarian cancer-associated protein #24.
 XX cyrostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
 KW post-operative chemotherapy; radiation therapy; tumour prognosis;
 KW pre-cancerous lesion detection.
 XX OS Homo sapiens.
 XX WO2002102235-A2.
 PN 27-DEC-2002.
 PD 18-JUN-2002; 2002WO-US019297.
 XX PR 18-JUN-2001; 2001US-0299234P.
 PR 27-AUG-2001; 2001US-0315284P.
 PR 05-SEP-2001; 2001US-0317544P.
 PR 13-NOV-2001; 2001US-0350664P.
 PR 12-APR-2002; 2002US-0372246P.
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

P1 Mack DH, Gish RC;
 XX WPI; 2003-167431/16.
 DR N-PSDB; ADB80483.
 XX Detecting an ovarian cancer-associated transcript in a cell from a
 PT patient, comprising contacting a biological sample from the patient with a
 PT polynucleotide that hybridizes to an ovarian cancer gene.
 XX Claim 13; Page 291; 332pp; English.
 XX The invention relates to a method of detecting an ovarian cancer-
 CC associated transcript in a cell from a patient, by contacting a
 CC biological sample from the patient with a polynucleotide that selectively
 CC hybridizes to a sequence at least 80% identical to any of one of 80
 CC nucleic acid sequences given in the specification. The method is useful
 CC in diagnosing ovarian cancer and in identifying and using agents and/or
 CC targets that inhibit ovarian cancer. The nucleic acid molecule,
 CC polypeptide and the antibody may also be used in detecting ovarian

CC cancers, monitoring and early detection of relapse following treatment,
 CC monitoring response to therapy, selecting patients for post-operative
 CC chemotherapy or radiation therapy, in selecting mode of therapy,
 CC determining tumour prognosis, early detection of pre-cancerous lesions,
 CC and as vaccines. This sequence corresponds to one of the proteins used
 XX for the detection method of the invention.

SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 7; Length 253;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLPLP 9
 Db 1 MARSLLPLP 9

RESULT 13
 AAB21326 standard; protein; 257 AA.
 XX AAB21326:
 AC AAB21326:
 XX XX 02-FEB-2001 (First entry)
 DE Human HSCCEB.
 XX Human KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; HSCCEB;
 KW human stratum corneum chymotryptic enzyme; kallikrein-like protein;
 KW serine protease; cytostatic; cancer; prostate cancer.
 AX OS Homo sapiens.
 XX WO20053776-A2.
 PN 09-MAR-2000; 2000WO-CA0000258.
 PD 14-SEP-2000.
 XX PR 09-MAR-2000; 2000WO-CA0000258.
 XX PR 11-MAR-1999; 99US-0124260P.
 PR 01-APR-1999; 99US-0127386P.
 PR 21-JUL-1999; 99US-0144919P.
 XX PA (MOUN) MOUNT SINAI HOSPITAL.
 XX PI Yousef GM, Diamandis EP;
 XX DR WPI; 2000-587440/55.
 XX PR New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
 PT protein mediated disorders, especially cancer.
 XX PS Example 4; Fig 17; 184pp; English.

XX The present sequence is human stratum corneum chymotryptic enzyme
 CC (HSCCEB), a member of the kallikrein multi-gene family. Kallikreins and
 CC kallikrein-like proteins are a subgroup of the serine protease enzyme
 CC family. They catalyze the selective cleavage of specific polypeptide
 CC precursors to release peptides with potent biological activity. Nucleic
 CC acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3,
 CC KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
 CC treatment, monitoring and diagnosis of cancers, especially prostate
 CC cancer. They can also be used to identify a substance that can associate
 CC with or mediate the biological activity of the proteins. Antibodies can
 CC be used to treat conditions mediated by the kallikrein-like proteins
 XX SQ Sequence 257 AA;

Query Match 100.0%; Score 41; DB 3; Length 257;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW antisthmatic; dermatological; antidiabetic; anti parkinsonian;
 KW antiinflammatory; antiulcer; antianginal; cardiotonic;
 KW hepatotropic; osteopathic; antidiabetic; antipyretic; viricide;
 KW antibacterial; fungicide; gastrointestinal; antidiarrhoeic; laxative;
 KW haemostatic; anti-HIV; thrombolytic; anticoagulant; gynaecological;
 KW cardiovascular; antiarterial; occlusive; hypotensive; vasotropic;
 KW anticancer; antirheumatic; immunosuppressive; antiallergic; antithyroid;
 KW nephrotoxic; antigout; thyromimetic; antiarthritis; urcopathic;
 KW ophthalmological; antiparasitic; tranquiliser; pulmonary; keratolytic;
 KW auditory; antiseborrhoeic; antidepressant; neuroleptic; antiinertial;
 KW antihelminthic; protozoacide; Crohn's disease; hypertension; autoimmune;
 KW inflammatory; anaemia; cell proliferative; developmental; epithelial;
 KW scabies; neurological; Alzheimer's disease; reproductive;
 KW ectopic pregnancy; gene therapy; vaccine; disorder; prostasin.
 XX OS Homo sapiens.
 XX WO200246383-A2.
 XX PD 13-JUN-2002.
 XX PF 05-DEC-2001; 2001WO-US046964.
 XX PR 08-DEC-2000; 2000US-0254399P.
 PR 21-DEC-2000; 2000US-0257803P.
 PR 05-JAN-2001; 2001US-0260110P.
 PR 19-JAN-2001; 2001US-0262851P.
 PR 25-JAN-2001; 2001US-0264423P.
 XX PA (INCYT) INCYTE GENOMICS INC.
 XX YUE, H., AZIMZAI, Y., KALLICK, DA., BAUGHN, MR., GRIFFIN, JA., SWARNAKAR, A.;
 PI LAI, PG., WALIA, NK., HAFAJIA, AJA., GANDHI, AR., AU-YOUNG, J., ELLIOT, VS.;
 PI RAMKUMAR, J., THANGAVELU, K., LU, Y., WARREN, BA., LU, DAM., LEE, EA.;
 PI TRIBBLEY, CM., ARVIZU, C., DELEGEANTE, AM., YAO, MG., KHAN, FA.;
 PI SANJAWALA, MM.;
 XX WPI; 2002-519664/55.
 DR N-PSDB; ABQ7956.
 XX PT New isolated Protein Modification and Maintenance polypeptides, useful
 PT for diagnosis, and treatment of e.g. Gastrointestinal disorders.
 XX PS Claim 1 (a); Page 174-176; 200PP; English.
 XX The invention relates to an isolated Protein Modification and Maintenance
 CC (PMM) polypeptide. Polypeptides of the invention may be used in the
 CC diagnosis, treatment and prevention of disorders associated with
 CC decreased expression or activity of PMM. These include gastrointestinal
 CC disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. anaemia), cell
 CC hypertension), autoimmune/inflammatory disorders (e.g. Alzheimer's disease),
 CC proliferative disorders, developmental disorders, epithelial disorders
 CC (e.g. scabies), neurological disorders (e.g. ectopic pregnancy) and in gene therapy or a
 CC vaccine for such diseases. They may also be used in the assessment of the
 CC effects of exogenous compound on the expression of nucleic acid and amino
 CC acid sequences of protein modification and maintenance molecules. The
 CC current sequence represents a human PMM of the invention, which has been
 CC found to have homology with rat prostasin
 XX Sequence 818 AA;
 SQ Score: 36; DB: 5; Length: 818;
 CC Q347: March 2002

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 1, 2004, 17:21:46 ; Search time 11.889 seconds
 39.081 Million cell updates/sec

Title: US-09-905-083-86
 Perfect score: 41
 Sequence: 1 MARSLLPL 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued Patents AA;*

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 2: /cgns_6/ptcdat/2/iaa/5B_COMBO.pep:
 3: /cgns_6/ptcdat/2/iaa/6A_COMBO.pep:
 4: /cgns_6/ptcdat/2/iaa/6B_COMBO.pep:
 5: /cgns_6/ptcdat/2/iaa/PCRS_COMBO.pep:
 6: /cgns_6/ptcdat/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	US-09-502-600-86	Sequence 86, Appl
2	41	100.0	9	US-09-918-243-86	Sequence 86, Appl
3	41	100.0	253	US-08-557-146-2	Sequence 2, Appl
4	41	100.0	253	US-08-824-874-3	Sequence 3, Appl
5	41	100.0	253	US-09-154-344-2	Sequence 2, Appl
6	41	100.0	253	US-08-930-188-2	Sequence 2, Appl
7	41	100.0	253	US-09-210-084-3	Sequence 3, Appl
8	41	100.0	253	US-09-764-762-3	Sequence 3, Appl
9	41	100.0	253	PCT-US96-04224-2	Sequence 2, Appl
10	36	87.8	9	US-09-600-116	Sequence 116, Appl
11	36	87.8	9	US-09-918-241-116	Sequence 116, Appl
12	35	85.4	518	US-09-939-723-2	Sequence 2, Appl
13	35	85.4	518	US-09-434-421-2	Sequence 2, Appl
14	35	85.4	518	US-09-548-372D-2	Sequence 2, Appl
15	35	85.4	518	US-09-549-356D-2	Sequence 2, Appl
16	35	85.4	518	US-09-551-855D-2	Sequence 19, Appl
17	35	85.4	518	US-09-215-450-19	Sequence 355, Appl
18	32	78.0	43	US-09-149-471-355	Sequence 3659, Appl
19	32	78.0	204	US-09-114-000C-3659	Sequence 485, Appl
20	32	78.0	238	US-09-149-476-485	Sequence 2, Appl
21	32	78.0	303	US-08-983-950-2	Sequence 2, Appl
22	32	78.0	303	US-09-546-049-2	Sequence 3072, Appl
23	32	78.0	493	US-09-25-991A-30722	Sequence 177, Appl
24	32	78.0	654	US-09-907-79A-177	Sequence 177, Appl
25	32	78.0	654	US-09-905-122A-177	Sequence 177, Appl
26	32	78.0	654	US-09-90-77A-177	Sequence 177, Appl
27	31	75.6	23	US-08-353-751-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
 US-09-502-600-86
 ; Sequence 86, Application US/09502600A
 ; Patent No. 6293344
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer
 ; FILE REFERENCE: D6223CIP/C
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/502,600A
 ; PRIOR FILING DATE: 03-14-1998
 ; NUMBER OF SEQ ID NOS: 136
 ; SEQ ID NO: 86
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Residues 1-9 of the SCC3 protein

RESULT 2
 US-09-918-243-86
 ; Sequence 86, Application US/09918243
 ; Patent No. 6627403
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; APPLICANT: Cannon, Martin J.
 ; APPLICANT: Santini, Alessandro
 ; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 ; FILE REFERENCE: D6223CIP/C/D/CIP
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/918,243
 ; PRIOR FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 136
 ; SEQ ID NO: 86
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

FEATURE: NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 1-9 of the SCCE protein
 US-09-918-243 86

Query Match Score 41; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3 US-08-557-146-2
 Sequence 2, Application US/08557146
 Patent No. 5834290
 GENERAL INFORMATION:
 APPLICANT: Egelrud, Torbjorn
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCE: 17
 TITLE OF INVENTION: Enzyme (SCCE)
 CORRESPONDENCE ADDRESS:
 STREET: White & Case, Patent Department
 CITY: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REFERENCE NUMBER: 35,372
 REGISTRATION NUMBER: 1103326-18A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-557-146-2

Query Match Score 41; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.32e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4 US-08-824-874-3
 Sequence 3, Application US/08824874
 Patent No. 59622300
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5

FEATURE: NAME/KEY: CHAIN.
 OTHER INFORMATION: Incyte Pharmaceuticals, Inc.
 US-09-918-243 86

Query Match Score 41; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5 US-09-154-244-2
 Sequence 2, Application US/09154344
 Patent No. 5981256
 GENERAL INFORMATION:
 APPLICANT: Egelrud, Torbjorn
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: White & Case, Patent Department
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/154,344
 FILING DATE: 16-SEP-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION:
 NAME: Stern, Richard J.
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 35,372
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 MOLECULE TYPE: Protein

US-09-914-344-2

Query Match Score 41; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSILPL 9
 Db 1 MARSILPL 9

RESULT 7
 US-09-210-084-3
 Sequence 3, Application US/09210084
 Patent No. 6197511
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 ATTORNEY: Lal, Preeti
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/210,084
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/824,874
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0252 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555;
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 532504

US-09-210-084-3

Query Match Score 41; DB 3; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSILPL 9
 Db 1 MARSILPL 9

RESULT 8
 US-09-164-762-3
 Sequence 3, Application US/09764762
 Patent No. 6472195
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 ATTORNEY: Lal, Preeti
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/764,762
 FILING DATE: 16-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE DOCKET NUMBER: FF-0252 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4146

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 532504

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-764-762-3

Query Match Score 41; DB 4; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
 Db 1 MARSLLPL 9

RESULT 9
 PCT-US96-04294-2
 Sequence 2, Application PC/TUS9604294
 GENERAL INFORMATION:
 APPLICANT: Dixon, Eric P.
 APPLICANT: Johnstone, Edward M.
 APPLICANT: Little, Sheila P.
 TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
 TITLE OF INVENTION: RELATED NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESS: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: United States of America
 ZIP: 46285

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/04294
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/416,257
 FILING DATE: 04-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Blalock, Donna K.
 REGISTRATION NUMBER: 38,082
 REFERENCE/DOCKET NUMBER: X9239
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-277-1090
 TELEFAX: 317-277-3861
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-04294-2

Query Match Score 41; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
 Db 1 MARSLLPL 9

RESULT 10
 US-09-502-600-116
 Sequence 116, Application US/09502600A
 Patent No. 6394344
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 Ovarian Cancer
 FILE REFERENCE: D6223CIP-C
 CURRENT FILING DATE: 2000-02-11
 CURRENT APPLICATION NUMBER: US/09/502,600A
 PRIOR APPLICATION NUMBER: 09/039,211
 PRIOR FILING DATE: 03-14-1998
 NUMBER OF SEQ ID NCS: 136
 SEQ ID NO: 116
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Residues 2-10 of the SCCE protein
 US-09-502-600-116

Query Match Score 36; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;

Qy 2 ARSLLPL 9
 Db 1 ARSLLPL 8

RESULT 11
 US-09-918-243-116
 Sequence 116, Application US/09918243
 Patent No. 6627403
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the early diagnosis of ovarian cancer
 FILE REFERENCE: D6223CIP/C/DCIP
 CURRENT APPLICATION NUMBER: US/09/918,243
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US
 PRIOR FILING DATE: 2001-07-13
 PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 136
; SEQ ID NO: 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
us-09-918-43-116

Query Match 87.8%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 2 ARSLLPL 9
Db 1 ARSLLPL 8

RESULT 14
US-09-548-372D-2
; Sequence 2, Application US/09548372D
; Patent No. 6420334
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548-372D
; CURRENT FILING DATE: 2000-04-12
; PRIORITY NUMBER: US 60/155,493
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIORITY NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; PRIORITY NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-372D-2

Query Match 85.4%; Score 35; DB 4; Length 518;
Best Local Similarity 77.8%; Pred. No. 14; 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0; Indels 0;

Qy 1 MARSLLPL 9
Db 4 LARALLPL 12

RESULT 15
US-09-548-367D-2
; Sequence 2, Application US/09548367D
; Patent No. 6440688
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548-367D
; CURRENT FILING DATE: 2000-04-12
; PRIORITY NUMBER: US 60/155,493
; PRIOR APPLICATION NUMBER: 1999-01-23
; PRIORITY NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; PRIORITY NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-548-367D-2

RESULT 13
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022, 9
; EARLIER FILING DATE: 1996-12-14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-434-427-2

Query Match 85.4%; Score 35; DB 4; Length 518;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0;
Matches 0; Gaps 0;

Qy 1 MARSILLPL 9
Db 4 LARALLEPL 12

Search completed: March 1, 2004, 17:38:26
Job time : 12.8889 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:35:01 ; Search time 24.1111 seconds

(without alignments)

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Title: US-09-905-083-86

Perfect score: 41

Sequence: 1 MARSILPL 9

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Maximum Match 10.0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	41	100.0	9	9	US-09-918-243-86	Sequence 86, App1
2	41	100.0	9	9	US-0-915-083-86	Sequence 86, App1
3	41	100.0	253	9	US-09-888-615-98	Sequence 98, App1
4	41	100.0	253	9	US-09-764-762-3	Sequence 3, App1
5	41	100.0	253	14	US-10-264-283-90	Sequence 90, App1
6	41	100.0	253	15	US-10-295-07-498	Sequence 498, App1
7	41	100.0	253	15	US-10-173-989-48	Sequence 48, App1
8	36	87.8	9	9	US-09-918-243-86	Sequence 116, App
9	36	87.8	9	9	US-0-905-083-116	Sequence 116, App
10	36	87.8	818	9	US-09-888-615-111	Sequence 111, App
11	35	85.4	518	9	US-09-794-927-2	Sequence 2, App1
12	35	85.4	518	9	US-09-795-847-2	Sequence 2, App1
13	35	85.4	518	9	US-09-734-743-2	Sequence 2, App1
14	35	85.4	518	9	US-09-794-748-2	Sequence 2, App1
15	35	85.4	518	9	US-09-734-925-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-918-243-86

; Sequence 86, Application US/09918243

; GENERAL INFORMATION:

; APPLICANT: O'Brian, Timothy J.

; CANNON, Martin J.

; ATTORNEY: Santini, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D62223CIP/C/D/CP

; CURRENT APPLICATION NUMBER: US-09/918-243

; PRIORITY APPLICATION NUMBER: US-

; PRIOR FILING DATE: 2001-07-30

; PRIORITY FILING DATE: 2001-07-13

; SEQ ID NO: 86

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 1-9 of the SCCE protein

US-09-918-243-86

; Query Match 100.0%; Score 41; DB 9; Length 9;

; Best Local Similarity 100.0%; Pred. No. 7.1e+05;

; Mismatches 0; Indels 0; Gaps 0;

; RESULT 2
US-09-905-083-86

; Sequence 86, Application US/09905083

; PATENT NO. US-0020046708A1

; GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
 Title of Invention: Ovarian Cancer

FILE REFERENCE: D623CIP/C/Div
 CURRENT APPLICATION NUMBER: US/09/905,083
 PRIORITY NUMBER: US 09/502,600
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 136
 SEQ ID NO: 86
 LENGTH: 9

TYPE: PRT
 ORGANISM: Homo sapiens

FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Residues 1-9 of the SCCE protein

US-09-905-083-86

Query Match 100.0%; Score 41; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSILPL 9
 Db 1 MARSILPL 9

RESULT 3
 US-09-888-615-98
 Sequence 98 Application US/09888615
 Patent No. US2002006456A1
 GENERAL INFORMATION:
 APPLICANT: PLUMMAN, GREGORY
 APPLICANT: WHYTE, DAVID
 APPLICANT: CAENEPEEL, SEAN
 APPLICANT: CHARYDZAK, GLEN
 APPLICANT: MANNING, GERARD
 APPLICANT: SUDARSANAM, SUCHA
 TITLE OF INVENTION: NOVEL PROTEASES
 FILE REFERENCE: 03602/12/14
 CURRENT APPLICATION NUMBER: US/09/888,615
 CURRENT FILING DATE: 2001-06-26
 PRIOR APPLICATION NUMBER: 60/214,047
 PRIOR FILING DATE: 2000-06-26
 NUMBER OF SEQ ID NOS: 150
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 98
 LENGTH: 253

TYPE: PRT
 ORGANISM: Homo sapiens

US-09-888-615-98

Query Match 100.0%; Score 41; DB 9; Length 253;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSILPL 9
 Db 1 MARSILPL 9

RESULT 4
 US-09-764-762-3
 Sequence 3 Application US/09764762
 Patent No. US2002006834A1
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 Lal, Preeti
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 STREET: 3174 Porter Drive
 ADDRESSEE: Incyte Pharmaceuticals, Inc.

CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORMATTE
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/764,762
 FILING DATE: 16-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/210,084
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: PP-0252 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-1555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 53304
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-764-762-3

Qy 1 MARSILPL 9
 Db 1 MARSILPL 9

RESULT 5
 US-10-264-283-90
 Sequence 90 Application US/10264283
 Publication No. US20030144494A1
 GENERAL INFORMATION:
 APPLICANT: Aligate, Paul A.
 APPLICANT: Mannion, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 210121,590
 CURRENT APPLICATION NUMBER: US/10/264,283
 CURRENT FILING DATE: 2002-10-02
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: Corixa Invention Disclosure Database
 SEQ ID NO: 90
 LENGTH: 253
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-264-283-90

Qy 1 MARSILPL 9
 Db 1 MARSILPL 9

RESULT 6
US-10-295-027-498
Sequence 498, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
Aziz, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
Glynn, Richard
Hevezsi, Peter A.
Mack, David H.
Murray, Richard
Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
Title of Invention: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-0125000S
CURRENT APPLICATION NUMBER: US/10/295,027
PRIORITY APPLICATION NUMBER: US/10/295,027
PRIORITY FILING DATE: 2002-11-13
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: US 60/350,666
PRIORITY APPLICATION NUMBER: US 60/335,394
PRIORITY APPLICATION NUMBER: US 60/332,464
PRIORITY APPLICATION NUMBER: US 2001-11-21
PRIORITY FILING DATE: 2001-11-13
PRIORITY FILING DATE: 2001-11-15
PRIORITY FILING DATE: 2001-11-15
PRIORITY FILING DATE: 2001-11-29
PRIORITY FILING DATE: 2001-11-29
PRIORITY FILING DATE: 2001-12-14
PRIORITY FILING DATE: 2001-12-14
PRIORITY FILING DATE: 2002-01-08
PRIORITY FILING DATE: 2002-01-10
PRIORITY FILING DATE: 2002-02-08
PRIORITY FILING DATE: 2002-02-13
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NUMBER OF SEQ ID NOS: 1386
SEQ ID NO 498
SOFTWARE: PatentIn Ver. 2.1
TYPE: PPT
ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 41; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
Db 1 MARSLLPL 9

RESULT 7
US-10-173-999-498
Sequence 498, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
Gish, Kurt C.
Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions and
Title of Invention: Methods of Screening for Modulators of Ovarian
Title of Invention: Cancer
FILE REFERENCE: 018501-002401US
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234

Query Match 100.0%; Score 41; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.2;
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Qy 1 MARSLLPL 9
Db 1 MARSLLPL 9

RESULT 8
US-09-918-243-116
Sequence 116, Application US/09918243
Patent No. US2002014231A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
Cannon, Martin J.
Santini, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/DCIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 116
LENGTH: 9
TYPE: PPT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 2-10 of the SCCE protein

Query Match 87.8%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+03
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
Db 1 MARSLLPL 9

RESULT 9
US-09-905-083-116
Sequence 116, Application US/09905083
Patent No. US20020146708A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
Ovarian Cancer
FILE REFERENCE: D6223CIP/C/DCIP
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 116
LENGTH: 9

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; TYPE: PRT ; ORGANISM: Homo sapiens
; FEATURE: CHAIN
; NAME/KEY: SCCE
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-905-083-116
Query Match 87.8%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ARSILLPL 9
Db 1 ARSILLPL 8

.RESULT 10
US-09-888-615-111
; Sequence 111, Application US/09888615
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/8888, 615
PRIORITY APPLICATION NUMBER: 2001-06-26
PRIOR FILING DATE: 2000-06-26
SEQ ID NO: 111
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 838
TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-615-111
Query Match 87.8%; Score 36; DB 9; Length 818;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MARSHILLPL 9
Db 1 MARSHILLPL 8

.RESULT 11
US-09-794-927-2
; Sequence 2, Application US/09794927
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Biernkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280DE
CURRENT APPLICATION NUMBER: US/09/795, 847
PRIORITY APPLICATION NUMBER: 09/116, 901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155, 493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404, 133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101, 594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2
LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapiens
US-09-795-947-2
Query Match 85.4%; Score 35; DB 9; Length 518;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Indels 0; Gaps 0;
QY 1 MARSILLPL 9
Db 4 LARALLPL 12

.RESULT 12
US-09-795-847-2
; Sequence 2, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Biernkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280DE
CURRENT APPLICATION NUMBER: US/09/795, 847
PRIORITY APPLICATION NUMBER: 09/116, 901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155, 493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404, 133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101, 594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2
LENGTH: 518
TYPE: PRT
ORGANISM: Homo sapiens
US-09-795-947-2
Query Match 85.4%; Score 35; DB 9; Length 518;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Indels 0; Gaps 0;
QY 1 MARSILLPL 9
Db 4 LARALLPL 12

.RESULT 13
US-09-794-743-2
; Sequence 2, Application US/09794743
; Patent No. US2001002139A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Biernkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/794, 927
PRIORITY APPLICATION NUMBER: 09/416, 901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155, 493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404, 133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881

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TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 TITLE OF INVENTION: USES
 FILE REFERENCE: 28341/6280FC
 CURRENT FILING DATE: 2001-02-27
 PRIOR APPLICATION NUMBER: 09/416,901
 PRIOR FILING DATE: 1999-10-13
 PRIOR APPLICATION NUMBER: 60/155,493
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: 09/404,133
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: PCT/US99/20881
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: 60/101,594
 PRIOR FILING DATE: 1998-05-24
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2
 LENGTH: 518
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-794-743-2

Query Match 85.4%; Score 35; DB 9; Length 518;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 2; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
 Db 4 LARALLPL 12

RESULT 14
 US-09-794-748-2
 Sequence 2, Application US/09794748
 Patent No. US2002037315A1
 GENERAL INFORMATION:
 / APPLICANT: Gurney, Mark E.
 / APPLICANT: Bienkowski, Michael J.
 / APPLICANT: Heinrikson, Robert L.
 / APPLICANT: Yan, Riqiang
 / TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 / TITLE OF INVENTION: USES
 / FILE REFERENCE: 28341/6280FC
 / CURRENT FILING DATE: 2001-02-27
 / PRIOR APPLICATION NUMBER: 09/416,901
 / PRIOR FILING DATE: 1999-10-13
 / PRIOR APPLICATION NUMBER: 60/155,493
 / PRIOR FILING DATE: 1999-09-23
 / PRIOR APPLICATION NUMBER: 09/404,133
 / PRIOR FILING DATE: 1999-09-23
 / PRIOR APPLICATION NUMBER: PCT/US99/20881
 / PRIOR FILING DATE: 1999-09-23
 / PRIOR APPLICATION NUMBER: 60/101,594
 / PRIOR FILING DATE: 1998-09-24
 / NUMBER OF SEQ ID NOS: 73
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 2
 / LENGTH: 518
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-794-745-2

Query Match 85.4%; Score 35; DB 9; Length 518;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 2; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
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 Db 4 LARALLPL 12

Search completed: March 1, 2004, 18:08:53
 Job time : 25.1111 secs

RESULT 15
 US-09-794-925-2
 Sequence 2, Application US/09794925
 Patent No. US2002064819A1
 GENERAL INFORMATION:
 / APPLICANT: Gurney, Mark E.
 / APPLICANT: Bienkowski, Michael J.
 / APPLICANT: Heinrikson, Robert L.
 / APPLICANT: Parodi, Luis A.
 / TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 / TITLE OF INVENTION: USES
 / FILE REFERENCE: 28341/6280FC
 / CURRENT FILING DATE: 2001-02-27
 / PRIOR APPLICATION NUMBER: 09/416,901
 / PRIOR FILING DATE: 1999-10-13
 / PRIOR APPLICATION NUMBER: 60/155,493
 / PRIOR FILING DATE: 1999-09-23
 / PRIOR APPLICATION NUMBER: 09/404,133
 / PRIOR FILING DATE: 1999-09-23
 / PRIOR APPLICATION NUMBER: PCT/US99/20881
 / PRIOR FILING DATE: 1999-09-23
 / PRIOR APPLICATION NUMBER: 60/101,594
 / PRIOR FILING DATE: 1998-09-24
 / NUMBER OF SEQ ID NOS: 73
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 2
 / LENGTH: 518
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-794-78-2

Query Match 85.4%; Score 35; DB 9; Length 518;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 2; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSLLPL 9
 :|||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:21:01 ; search time 10.2222 Seconds
 84.690 Million cell updates/sec

Title: US-09-905-083-86
 Perfect score: 41

Sequence: 1 MARSLLPL 9

Scoring table: BLOSUM62
 Gapopen 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78;*

1: _pir1;*

2: _pir2;*

3: _pir3;*

4: _pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	1 41 100.0	253	2	A51968	serine proteinase
2	2 34 82.0	461	2	A63394	suppressor protein
3	3 33 80.5	397	2	B87343	conserved hypothetical prote
4	4 33 80.5	571	2	E94550	hypothetical prote
5	5 33 80.5	582	2	I48673	matrix metalloprote
6	6 33 80.5	582	2	I54471	matrix metalloprote
7	7 32 78.0	81	2	B91856	hypothetical prote
8	8 32 78.0	126	2	C8A169	DNA-binding prote
9	9 32 78.0	432	2	A81060	hypothetical prote
10	10 32 78.0	506	2	B87102	conserved membrane
11	11 32 78.0	921	2	T51136	ionotropic glutamate
12	12 32 78.0	923	2	F8732	probable ligand-ga
13	13 32 78.0	1628	2	T38055	hypothetical prote
14	14 31 75.6	138	2	I44107	sodium channel alp
15	15 31 75.6	147	2	S24698	hypothetical prote
16	16 31 75.6	169	2	B23016	cell division inhi
17	17 31 75.6	169	2	A80627	cell division inhi
18	18 31 75.6	294	2	B8A450	hypothetical prote
19	19 31 75.6	346	2	T11364	NADH dehydrogenas
20	20 31 75.6	375	2	C71917	probable transamin
21	21 31 75.6	375	2	H6597	probable transamin
22	22 31 75.6	452	2	A83134	PTS system, n-acet
23	23 31 75.6	491	2	JC6197	stronelysin
24	24 31 75.6	556	1	S31330	EC 3.2.1.-
25	25 31 75.6	708	2	T43109	inulinase
26	26 31 75.6	2005	2	B2019	cytoysin B transp
27	27 31 75.6	5089	2	T12464	sodium channel pro
28	28 30 73.2	72	2	JC2384	rifamycin Polypepti
29	29 30 73.2	74	2	T17834	coraonin precursor

ALIGNMENTS

RESULT 1

A53968

serine proteinase SCCE precursor - human

WAльтерни names: stratum corneum chymotryptic enzyme

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995

C;Accession: A53968

R.Hansson, L.; Stroemqvist, M.; Backman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.

J. Biol. Chem. 269, 19420-19422, 1994

A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym

A;Reference number: A53968; PMID:8034709

A;Accession: A53968

A;Molecule type: mRNA

A;Residues: 1-253 <HAN>

A;Cross-references: QB:L33404; PID:9521214; PIDN: AAC37551.1; PMID:9532504

C;Genetics:

A;Map position: 7q35-7q35

A;Cross-references: GDB:377730

F;30-245;Domain: trypsin homology <TRY>

RESULT 2

Qy

1 MARSLLPL 9

Db

1 MARSLLPL 9

1 MARSLLPL 9

Query Match 100.0%; Score 41; DB 2; Length 253;

Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C;Species: Saccharomyces cerevisiae

C;Accession: A46394; S64827

C;Date: 18-May-1994 #sequence_revision 19-Jul-1996

R.Yoon, H.; Miller, S.P.; Pabich, E.K.; Donahue, T.F.

Genes Dev. 6, 2463-2477, 1992

A;Title: SSSL, a suppressor of a HIS4 5'-UTR stem-loop mutation, is essential for transl

A;Reference number: A46394; PMID:94040711; PMID:1340463

A;Accession: A46394

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-461 <YOO>

A;Cross-references: GB:Z17385; NID:92695; PID:92696

R.Vandenbo, M.; Porteille, D.; Hilger, F.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64827

A;Accession: S64827

A;Molecule type: DNA
A;Residues: 1-461 <VAN>
A;Cross-references: EMBL:Z71177; NID:gi360293; PID:gi360294; MIPS:YLR005w
A;Note: experimental_source strain S288C
C;Genetics:
A;Gene: SGD:S011
A;Cross-references: SGD:S0003995; MIPS:YLR005w
A;Map position: 12R
C;Superfamily: RNA Polymerase II transcription initiation/nucleotide excision repair fac
C;Keywords: transmembrane protein
F;356-372/Domain: transmembrane #status predicted <TMM>

Query Match Score 34; DB 2; Length 461;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSIIPL 9
Db 216 MARGILLPV 224

RESULT 3
B87443
Conserved hypothetical Protein CCG0757 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: B87443
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, J.; Heidelberg, J.
B.; Laub, M.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:211259698; PMID:11259647
A;Accession: B87443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <STO>
A;Cross-references: GB:AE005673; NID:gi13421992; PIDN:AK22742.1; GSPDB:GN00148
C;Genetics:
A;Gene: CCG0757

Query Match Score 33; DB 2; Length 397;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSIIPL 9
Db 285 LARALIPL 293

RESULT 4
E96550
hypothetical protein F11M15.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-eared Cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96550
R;Theologis, E.; Ecker, J.R.; Palm, C.J.; Federediel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Devar, K.
ansen, N.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-571 <STO>
A;Cross-references: GB:AB005173; NID:gi4836937; PIDN:ADD30639.1; GSPDB:GN00141
C;Genetics:

RESULT 9
 P:61-284/Domain: matrix metalloproteinase homology <MPB>
 P:313-509/Domain: hemopexin repeat homology <PXN>
 P:93-139/243-249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 P:239-243-249/Binding site: zinc, catalytic (His) (active) #status predicted
 P:240/Active site: Glu #status Predicted

Query Match Similarity 80.5%;	Score 23;	DB 2;	Length 582;
Best Local Similarity 87.5%;	Pred. No. 45;	Indels 0;	Gaps 0;
Matches 7;	Conservative 1;	Mismatches 0;	
Qy 2 ARSLLPL 9	Db 8 SRSLLPL 15		

A;Accession: A83060
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-432 <STO>
 A;Cross-references: GB:AE004882; GB:AE004091; NID:99950939; PMID:10984043
 A;Experimental source: strain PA01
 C;Genetics:

A;Gene: PA4680

RESULT 7
 B97856 hypothetical protein RC1250 [imported] - Rickettsia conorii (strain Malish 7)
 C;Species: Rickettsia conorii
 C;Accession: B97856
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Sanson, D.; RC
 Science 293, 2003-2098, 2001
 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A;Reference number: A97700; MUID:21442074; PMID:11557893
 A;Accession: B97856
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-81 <KUR>
 A;Cross-references: GB:AE006914; PIDN:AA03788.1; PIDN:915620385; GSPDB:GN00173
 C;Genetics:
 A;Gene: RC1250

Query Match Similarity 78.0%; Score 32; DB 2; Length 81;
 Best Local Similarity 75.0%; Pred. No. 9.3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ARSLLPL 9	Db 43 ARSLLPI 50		
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A;Accession: B87102
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-506 <STO>
 A;Cross-references: GB:AL450380; NID:91393364; PIDN:CRAC30495.1; GSPDB:GN00147
 C;Genetics:

A;Gene: ML1544
 C;SuperFamily: Mycobacterium tuberculosis hypothetical protein Rv1782

Query Match Similarity 78.0%; Score 32; DB 2; Length 56;
 Best Local Similarity 77.8%; Pred. No. 63; Mismatches 7; Indels 0; Gaps 0;

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: B87102
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-506 <STO>
 A;Cross-references: GB:AL450380; NID:91393364; PIDN:CRAC30495.1; GSPDB:GN00147
 C;Genetics:

A;Gene: ML1544
 C;SuperFamily: Mycobacterium tuberculosis hypothetical protein Rv1782

Query Match Similarity 78.0%; Score 32; DB 2; Length 56;
 Best Local Similarity 77.8%; Pred. No. 63; Mismatches 7; Indels 0; Gaps 0;

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

RESULT 8
 C82169 DNA-binding protein inhibitor Id-2-related protein VC1696 [imported] - Vibrio cholerae
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: C82169
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Givnn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: C82169
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-126 <HEI>
 A;Cross-references: GB:AE004247;
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:

A;Map position: 1

Qy 1 MARSLLPL 8	Db 33 MARSLLIP 40		
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RESULT 11
 T51136 ionotropic glutamate receptor girs [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
 C;Accession: T51136
 R;Davenport, R.J.; Kiegle, E.A.; Tester, M.
 submitted to the EMBL Data Library, December 1999
 A;Description: GIRS, an ionotropic glutamate receptor ortholog from Arabidopsis.
 A;Accession: T51136
 A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-921 <DAV>
A;Cross-references: ENBL:AT210701; PIDN:AAF21042.1
A;Experimental source: cultivar Columbus
C;Genet-loc:
A;Gene: g1r5
A;Map position: 2

Query Match 78.0%; Score 32; DB 2; Length 921;
Best Local Similarity 77.8%; Pred. No. 1.e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSILPL 9
Db 707 MARSILPL 713

RESULT 12

F84732 probable ligand-gated ion channel subunit [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailor, J.;
M.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84732
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-923 <STO>
A;Cross-references: GB:AE002093; NID:53831456; PIDN: AAC693938.1; GSDB:GN00039
C;Genetics:
A;Gene: At2g32400
A;Map position: 2

Query Match 78.0%; Score 32; DB 2; Length 923;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSILPL 9
Db 707 MARSILPL 715

RESULT 13

T38055 hypothetical protein SPAC22F3.14c - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T38055; T38177; S62429
R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1995
A;Reference number: Z21765
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-26 <LY1>
A;Cross-references: EMBL:Z69239; PIDN:CAA93223.1; GSDB:GN00066; SPDB:SPAC1D4.14
R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21776
A;Molecule type: DNA
A;Residues: 8-126 <LY2>
A;Cross-references: EMBL:Z54285; NID:g1008429; PIDN:CAA91079.2; GSDB:GN00066; SPDB:SPAC1D4.14
A;Map Position: II

Query Match 78.0%; Score 32; DB 2; Length 1628;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RSILPL 9
Db 583 RSILPL 589

RESULT 14

I48107 sodium channel alpha subunit - long-tailed hamster (fragment)
C;Species: *Crictetus longicaudatus* (Long-tailed hamster)
C;Date: 02-Jul-1995 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I48107
R;Latik, P.H.; Krater, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-138 <RES>
A;Cross-references: GB:M87540; NID:g191067; PIDN:AAA36978.1; BID:G191068
C;Genetics:
A;Gene: ch01
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 75.6%; Score 31; DB 2; Length 138;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSILIP 8
Db 1 MARSILIP 8

RESULT 15

S28698 hypothetical protein 16 - Agrobacterium tumefaciens plasmid pTi15955
C;Species: Agrobacterium tumefaciens
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C;Accession: S28698
R;Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A;Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo
A;Reference number: S28693
A;Accession: S28698
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-147 <BAR>
A;Cross-references: EMBL:X00493; NID:g39062; PIDN:CAA25178.1; BID:g39078
C;Genetics:
A;Genome: plasmid

Query Match 75.6%; Score 31; DB 2; Length 147;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSILIP 8
Db 1 MARYLIP 8

Search completed: March 1, 2004, 17:36:32
Job time : 11.333 secs

cleaves insulin B chain at 6-Leu-1-Cys-7, 16-Tyr-1-Leu-17, 25-Phe-1-Tyr-26, and 26-Tyr-1-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

-!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Hominoidea; Homo. NCBI-TaxID=9606;

[1] SEQUENCE FROM N.A. MEDLINE:20057170; PubMed:10591213; Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A., Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B., Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.; "membrane-anchored aspartyl protease with Alzheimer's disease beta-secretase activity"; Nature 402:533-537(1999).

[2] SEQUENCE FROM N.A. TISSUE=bone marrow; Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.

DR SGD; S0003995; SSL1.
 DR InterPro; IPR004595; SSL1.
 DR InterPro; IPR007198; SSL1-like.
 DR InterPro; IPR007087; Znf_C2H2.
 DR PFam; PF04055; SSL1_1.
 DR SMART; SMC00155; Znf_C2H2_1.
 DR PROSITE; PS00028; Zinc FINGER_C2H2_1_1.
 DR PROSITE; PS00157; Zinc FINGER_C2H2_1_2; FALSE_NEG.
 DR Zinc-finger; Nuclear Protein; Metal_L-binding.
 FT ZN FING 427 449
 SEQUENCE 461 AA; 52290 MW; 57ADCB630B790B4F CRC64;

Query Match Score 82.9%; Score 34; DB 1; Length 461;
 Best Local Similarity 77.8%; Pred. No. 11; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1;

Qy 1 MARSLLPL 9
 Db 216 MARGILLPV 224

RESULT 4
 ID OTSA_RHISN STANDARD PRT; 464 AA.
 AC P55612;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming]
 (EC 2.4.1.15) (Trehalose-6-phosphate synthase) (UDP-glucose-
 Glucosidase)
 DE OTSA OR Y4Pc.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym phGR234A.
 BC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhiobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OC NCB_1_TaxID=394;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9161424;
 RA Freiberg C.A., Fellay R., Barroch A., Broughton W.J., Rosenthal A.,
 Perret X;
 RT "Molecular basis of symbiosis between Rhizobium and legumes."
 RL Nature 387:394-401(1997).
 CC -!- CATALYTIC ACTIVITY: UDP-Glucose + D-glucose 6-phosphate = UDP +
 alpha,alpha-trehalose 6-phosphate.
 CC -!- SIMILARITY: Belongs to the Glycosyltransferase family 20.
 CC -!- SIMILARITY: STRONG TO A NON-FUNCTION COPY IN NGR234, FQ1-FQ2,
 CC TRUNCATED BY A ISRM3-LIKE INSERTION ELEMENT.

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 or send an email to license@isb-sib.ch).

CC EMBL; AE000090; AAB91813_1; -.
 DR InterPro; IPR001830; Glyco_trans_20.
 DR PFam; PF000882; Glyco_trans_20_1.
 KW Transferase; Glycosyltransferase; Plasmid.

SQ SEQUENCE 464 AA; 51627 MW; 96D0610D739FA73 CRC64;

Query Match Score 80.5%; Score 33; DB 1; Length 464;
 Best Local Similarity 77.8%; Pred. No. 18; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1;

Qy 1 MARSLLPL 9
 Db 418 MARSLSMPL 426

RESULT 5
 ID MM14_MOUSE STANDARD PRT; 582 AA.
 AC P51690; 008645; 035369;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DT Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
 DB Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
 DE (Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MT1-MMP) (MMP-
 X1) (MT-MMP).
 GN MMP-14 OR MT-MMP.
 OS Mus musculus (Mouse).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] _
 RP SEQUENCE FROM N.A.
 RX MEDLINE=5224014; PubMed=7708715;
 RA Okada A., Bellucci J.P., Royer N., Chenard M.P., Rio M.C.,
 RA Chambo P., Bassat P.;
 RA "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in
 RST stromal cells of human colon, breast, and head and neck carcinomas."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995).
 RP REVISIONS.
 RA Odaka A.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3] _
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9325265;
 RX MEDLINE=9467335; PubMed=9325265;
 RA Apté S.S., Fukai N., Beier D.R., Olsan B.R.;
 RA "The matrix metalloproteinase-14 (MMP-14) gene is structurally
 RST distinct from other MMP genes and is co-expressed with the TIMP-2 gene
 during mouse embryogenesis."
 RL J. Biol. Chem. 272:25511-25517(1997).
 RP [4] _
 RN SEQUENCE FROM N.A.
 RX STRAIN=CD-1; TISSUE=Kidney;
 RX MEDLINE=90311877; PubMed=9648071;
 RA Kashiwara N., Wallner E.I., Kanwar Y.S.;
 RA Steetler-Stevenson W.G., Yang Q., Kumar A., Wada J.,
 RA Ward J.M., Birckel-Hansen H.;
 RA Cell 99:81-92 (1999).
 RT -!- FUNCTION: Endopeptidase that degrades various components of the
 extracellular matrix, such as collagen. Activates proteoglycans A,
 essential for pericellular collagenolysis and modeling of skeletal
 and extraskelatal connective tissues during development.
 CC -!- CATALYTIC ACTIVITY: Endopeptidase activity. Activates
 progelatinase A by cleavage of the propeptide domain.
 CC Other bonds hydrolyzed include 35'-Gly-Lle-16 in the propeptide
 CC of collagenase 3, and 341-Asn-L-Phe-342, 441-Asp-L-Leu-442 and
 CC 356-Glu-L-Trp-355 in the aggrecan interglobular domain.
 CC -!- COFACTOR: Binds 1 ion per subunit, calcium (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, kidney, heart,
 CC lung, embryonic skeletal and periosteal tissues.
 CC -!- DEVELOPMENTAL STAGE: Not detected before day 10.5. At day 12.5,
 CC prominently expressed in large arteries and the umbilical

arteries, expressed at lower levels in the myocardium, craniofacial mesenchyme, nasal epithelium and liver capsule. At days 14.5 and 17.5, expressed in the musculoskeletal system, and ossification areas, with continued expression in the arterial tunica media.

-|- PRM: The precursor is cleaved by a furin endopeptidase (By similarity).

-|- SIMILARITY: Belongs to peptidase family M10A.

-|- SIMILARITY: Contains 1 hemopexin-like domain.

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	Query Match	Match Similarity	Score	DB 1;	Length	582;
	Best	Local Similarity	33;	Pred. No.	23;	
	Matches	7;	Mismatches	1;	Indels	0;
					Gaps	0;
CC	QY	2 ARSLILPL 9				
CC	DB	: :				
CC		8 SRSLLPL 15				
<hr/>						
RESULT 6						
MM14_RAT	MM14_RAT	STANDARD;	PRT;	582 AA.		
ID Q10739; DT 01-OCT-1996 (Rel. 34, Created)						
DT 01-OCT-2003 (Rel. 42, Last annotation update)						
DE Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)						
DE (Membrane-type matrix metalloproteinase 1) (MT1-MMP) (MT1-MMP) (MT1-MMP)						
DE (Membrane-type-1 matrix metalloproteinase)						
DE MMP14 OR MMMP.						
GN Rattus norvegicus (Rat).						
OS Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;						
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.						
NCBI_TaxID:10116;						
DE [1]						
RN SEQUENCE FROM N.A.						
RP MEDLINE=9522401; PubMed=7708715;						
RA Okada A.; Bellod G.P.; Rouyer N.; Chenard M.P.; Rio M.C.,						
RA Chamberon P.; Basset P.;						
RA "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells of human colon, breast, and head and neck carcinomas." Proc. Natl. Acad. Sci. U.S.A. 92:230-234 (1995).						
RL [2]						
RN SEQUENCE FROM N.A.						
CC Cossins J., Clements J., Catlin G., Wells G.; Submitted (SEB-1995) to the EMBL/GenBank/DBJ databases.						
CC - - FUNCTION: Seems to specifically activate progelatinase A. May thus trigger invasion by tumor cells by activating progelatinase A on the tumor cell surface.						
CC - - CATALYTIC ACTIVITY: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at 37-Asn- -Leu-38. Other bonds hydrolyzed 3, and 341-Asn- -Leu-342, 441-Asp- -Leu-42 and 354-Gln- -Thr-355 in the aggrecan interglobular domain.						
CC - - COFACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).						
CC - - SUBCELLULAR LOCATION: Type I membrane protein (Potential).						
CC - - SIMILARITY: Belongs to peptidase family M10A.						
CC - - SIMILARITY: Contains 1 hemopexin-like domain.						
<hr/>						
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CC EMBL; X81537; CAA58521_1; -.						
CC EMBL; X91785; CRA2897_1; -.						
CC PIR; I84471; 184471.						
CC HSSP; P08254; 1HFS.						
CC MEROPS; M10.014; -.						
CC InterPro; IPR000565; Hemopexin.						
CC InterPro; IPR001818; Pept_M10A_M12B.						
CC InterPro; IPR006035; Pept_M_Zn_BS.						
CC InterPro; IPR006036; Peptidase_M.						
CC Pfam; PF00045; hemopexin_4.						
CC Pfam; PF00413; Peptidase_M10_N.						
CC Pfam; PF03933; Peptidase_M10.						
CC SMART; SM00120; HX_4.						
DR PROSITE; PS00024; HEMOPEXIN_1.						
DR PROSITE; PS00142; ZINC PROTEASE_1.						
DR PROSITE; PS00546; CYSTEINE_SWITCH_1.						
KW Hydrolase; Metallopeptidase; Zinc; Zymogen; Calcium; Signal; Transmembrane; Collagen degradation; Extracellular matrix.						
KW SIGNAL 1 20						
FT PROPEP 21 111						
FT CHAIN 112 582						
FT DOMAIN 112 542						
FT TRANSMEM 563 562						
FT DOMAIN 316 511						
FT SITE 93 93						
FT METAL 239 239						
FT ACT SITE 240 240						
FT METAL 243 243						
FT DISULFID 249 249						
FT CONFLICT 319 508						
FT CONFLICT 133 133						
FT CONFLICT 255 255						
FT CONFLICT 258 258						
FT CONFLICT 341 341						
FT CONFLICT 346 346						
FT CONFLICT 378 378						
FT CONFLICT 390 391						
FT CONFLICT 400 401						
FT CONFLICT 407 407						
FT CONFLICT 412 412						
FT CONFLICT 417 417						
FT CONFLICT 512 512						
FT CONFLICT 512 512						
SQ SEQUENCE 65935 NW;						
SQ 3AB355158D4DD175 CRC64;						

"RGS-PXI, a GAP for Galphas and a sorting nexin in vesicular trafficking.", Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

RT SEQUENCE OF 607-968 FROM N.A.
MEDLINE21378165; PubMed=11485546;
RA Teasdale R.D., Loci D., Houghton F., Karlsson L., Gleeson P.A./
"A large family of endosome-localized proteins related to sorting
nexin 1".
RT Biochem. J. 358:9-16(2001).
RN TISSUE OF 651-968 FROM N.A.
RP SEQUENCE=placenta;
RC MEDLINE=22338257; PubMed=12477932;
RA Straubhaar R.L., Beigold P.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Colins F.S., Wagner L., Shemesh C.M., Bhattacharya S.,
Altschul S.F., Zeeberg B.H., Buetow K.H., Schuster A., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang G.J., Hsieh F.,
Ditachenko L., Mansuria K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshikyu S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McBewan P.J., McKernan K.J., Malek J.J., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Paehey J., Helton R., Kettman M., Madan A., Young A.C., Shevchenko A.,
Whiting M., Madan A., Rodriguez S., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimewood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

CC !- FUNCTION: May be involved in several stages of intracellular
trafficking. Act as a GAP for Galphas.
CC -! ALTERNATIVE PRODUCTS: Named isoforms=2;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y5W8-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Y5W8-2; Sequence=VSP_006192;
CC Note=No experimental confirmation available;
CC !- SIMILARITY: Belongs to the sorting nexin family.
CC !- SIMILARITY: Contains 1 RGS domain.
CC !- SIMILARITY: Contains 1 Pox homology (PX) domain.
CC !- SIMILARITY: Contains 1 PXA domain.
CC !- SIMILARITY: Ref.1 sequence differs from that shown due to a
framingshift in position 87.

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or send an email to license@isb-sib.ch).
CC EMBL; AB018256; BM3433.1; ALT_FRAME.
DR EMBL; AA420470; AAL37728.1; --.
DR EMBL; AB121882; ADD27335.1; --.
DR EMBL; BC022050; AAH22060.1; ALT_INIT.
DR Genew; FGNC:21335; SNX13.
DR MIM; 60589; --.
DR InterPro; IPR001683; PX.
DR InterPro; IPR003114; PX_assoc.
DR InterPro; IPR00312; Reg1_Sprotein.
DR Pfam; PF00787; PX_1.
DR Pfam; PF02194; PXA_1.
DR SMART; SM00615; RGS_1.
DR SMART; SM00312; PX_1.
DR SMART; SM00313; PXA_1.
DR SMART; SM00315; RGS_1.

DR PROSITE; PS50195; PX_1.
DR PROSITE; PS50132; RGS_1.
KW Transport: Protein transport; Signal transduction inhibitor;
KW Alternative splicing.
FT DOMAIN 97 284
FT DOMAIN 373 496
FT DOMAIN 570 691
FT VARSPLIC 569 579
FT CONFLICT 638 638
SQ SEQUENCE 968 AA; 112188 MW; 5329394AE0347FB5 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 968;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MARSIIPL 9
Db 254 LARGIIPL 262

RESULT 9
NAME=YATE_SCHPO STANDARD
ID=YATE_SCHPO
PRT: 1628 AA.
AC Q01779; OJ3884;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein C1D4_14 in chromosome I.
GN SPAC14.14 OR SPA2CF3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomyces; Schizosaccharomyces; Schizosaccharomyces; Schizosaccharomyces.
OC Schizosaccharomyces.
OC Schizosaccharomyces.
OX NCBI_TAXID4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=2148401; PubMed=11859360;
RX MEDLINE=2148401; PubMed=11859360;
RA Wood V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peart N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Monie S., Mungall K., Murphy J., Rabbinkowitz E.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinkowitz E.,
RA Rutherford K., Rutten S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkhardt G., Art R., Robben J., Grymonpre B.,
RA Weltjens I., Vanstraelen B., Rieger M., Scheffer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhartz R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wautbutt S., Purnelle B.,
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Leilaure V., Mottier S.,
RA Galibert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Roche M., Gallard C., Talleda V.A., Gazon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT Nature 415:871-880(2002).
RL -! SIMILARITY: Belongs to the THOC2 family.

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RT Comparisons among four closely related mammalian species-pairs.";
 RL J. Mol. Evol. 43:48-63 (1996).
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane; Belongs to the complex I subunit 2 family.

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CC EMBL; X03337; CAA27287.1; -.
 DR PIR; T11364; T11364.
 DR InterPro; IPR003917; NADHub_oxred2.
 DR InterPro; IPR001756; Oxidored_QI.
 DR Pfam; PF00361; oxidored_q1_1.
 DR PRINTS; PRO1436; NADHDIGNASE2.
 DR OXIDREDUCASE; NADH; Ubiquinone; Mitochondrion; Transmembrane.
 SQ SEQUENCE 346 AA; 38870 MW; 021D6D976DB564DB CRC64;

	Query Match	Score	31;	DB	1;	Length	346;
Qy	Best Local Similarity	75.6%		Pred. No.	37;		
Ds	Matches	7;	Conservative	1;	Mismatches	1;	Indels
						0;	Gaps
						0;	

RESUL.T 12
 CIN2_RAT STANDARD PRT; 2005 AA.
 ID CIN2_RAT
 AC P04775;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Sodium channel protein type II alpha subunit (Sodium channel protein, brain II alpha subunit).
 SCN2A.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. MEDLINE=B6146901; PubMed=3754035;

RX RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M., Takashita H., Numa S.; "Existence of distinct sodium channel messenger RNAs in rat brain."; Nature 320:188-192 (1986).
 CC -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
 CC -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1, S2, S3, S5, S6), and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
 CC -!- SIMILARITY: Belongs to the sodium channel family.
 CC -!- SIMILARITY: Contains 1 IQ domain.

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 CC EMBL; X03337; CAA27287.1; -.
 DR PIR; T11364; T11364.
 DR InterPro; IPR001682; Ca/Na_Pore.
 DR InterPro; IPR002111; Cat_channel_TrPL.
 DR InterPro; IPR00821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_lnlg.
 DR InterPro; IPR01196; Na_channelT.
 DR InterPro; IPR003915; PKD_2.
 DR Pfam; PF00520; ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR PRINTS; PRO1433; POLYCYSTIN2.
 DR SMART; SM00015; IQ_1.
 DR PROSITE; PS50036; IQ_1.
 KW Glycoprotein; Repeat; Multigene family; 3D-structure; Sodium channel;
 KW REPEAT; 111; 456.
 FT REPEAT; 111.
 FT REPEAT; 741; 1013.
 FT REPEAT; 1190; 1504.
 FT REPEAT; 1513; 1811.
 FT REPEAT; 157; 176.
 FT TRANSHM; 157; 176.
 FT TRANSHM; 190; 208.
 FT TRANSHM; 215; 234.
 FT TRANSHM; 251; 274.
 FT TRANSHM; 402; 427.
 FT TRANSHM; 754; 778.
 FT TRANSHM; 790; 813.
 FT TRANSHM; 822; 841.
 FT TRANSHM; 848; 867.
 FT TRANSHM; 884; 904.
 FT TRANSHM; 958; 983.
 FT TRANSHM; 1204; 1227.
 FT TRANSHM; 1241; 1266.
 FT TRANSHM; 1273; 1294.
 FT TRANSHM; 1340; 1367.
 FT TRANSHM; 1447; 1473.
 FT TRANSHM; 1527; 1550.
 FT TRANSHM; 1562; 1585.
 FT TRANSHM; 1592; 1615.
 FT TRANSHM; 1626; 1647.
 FT TRANSHM; 1663; 1685.
 FT TRANSHM; 1752; 1776.
 FT DOMAIN; 1905; 1934.
 FT CARBOHYD; 212; 212.
 FT CARBOHYD; 285; 285.
 FT CARBOHYD; 291; 291.
 FT CARBOHYD; 297; 297.
 FT CARBOHYD; 303; 303.
 FT CARBOHYD; 308; 308.
 FT CARBOHYD; 340; 340.
 FT CARBOHYD; 604; 604.
 FT CARBOHYD; 624; 624.
 FT CARBOHYD; 883; 883.
 FT CARBOHYD; 1055; 1055.
 FT CARBOHYD; 1072; 1072.
 FT CARBOHYD; 1136; 1136.
 FT CARBOHYD; 1382; 1382.
 FT CARBOHYD; 1393; 1393.
 SQ SEQUENCE 2005 AA; 227872 MW; 861BES83D79FB324 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 2005;
 Best Local Similarity 75.0%; Pred. No. 2,1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARSILP 8
Db 1 MARSILVLP 8
OC Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriodea; Drosophilidae; Drosophila.
NCB_TAXID=7227;

RESULT 13

CYTC_RABBIT STANDARD; PRT; 148 AA.
ID CYTC_RABBIT
AC 097862;
DT 16-OCT-2001 (Rel. 4.0, Created)
DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
DT 28-FEB-2003 (Rel. 4.1, Last annotation update)

DB Cystatin C Precursor.
GN CS3.

OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eutheria; Elegomorpha; Leporidae; Oryctodagus.
OX NCBI_TAXID=9986;

RN "Large scale isolation of osteoclast-specific genes by an improved
method involving the preparation of a subtracted cDNA library.";
RA Kobori M., Ikeda Y., Nara H., Kato M., Kumegawa M., Nojima H.,
RA Kawashima H.;
RT "Large scale isolation of osteoclast-specific genes by an improved
method involving the preparation of a subtracted cDNA library.";
RL Genes Cells 3:459-475(1998).
CC |- FUNCTION: This is a thiol proteinase inhibitor.
CC |- SIMILARITY: Belongs to the cystatin family.

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CC EMBL; AB009342; BAB75921.1; -.
DR HSSP; P01034; IG96.
DR InterPro; IPR00001; Cystatin.
DR Pfam; PF00031; Cystatin; 1.
DR SMART; SM00043; CR; 1.
DR PROSITE; PS00287; CYSTATIN; FALSE_NEG.
KW Thiol protease inhibitor; Signal.

FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 148 CYSTATIN C.
FT ACT SITE 39 39 REACTIVE SITE.
FT SITE 83 87 SECONDARY AREA OF CONTACT.
FT DISULFID 101 111 BY SIMILARITY.
FT DISULFID 125 145 BY SIMILARITY.
SQ SEQUENCE 148 AA; 16346 MW; 1523CB31169E59A CRC64;

Query Match 73.2%; Score 30; DB 1; Length 148;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSILP 9
Db 1 MARSILVLP 9

RESULT 14
CORZ_DRONE STANDARD; PRT; 154 AA.
ID CORZ_DRONE
AC Q26377; Q9VFK7;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Crz precursor [Contains: Corazonin; Corazonin-precursor-related
peptide (CPBP)].
DE CRZ OR CG3302.
GN Drosophila melanogaster (Fruit fly).

OS

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriodea; Drosophilidae; Drosophila.
NCB_TAXID=7227;

[1]

SEQUENCE FROM N.A.
STRAIN=Berkley;
MEDLINE=20198006; PubMed=10731132;
RN Adams M.D., Celinker S.E., Evans C.A., Gocayne J.D., Galle R.F.,
RA Amanatides P.G., Scheerer S.E., Li P.W., Hoskirk S.R.A., Gallo R.F.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wormser J.R., Yandell M.D., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaejel R.G., Champé M., Preiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.J.F., Agbayani A., An H.-J., Andrews P.Franklin C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Basiley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhardwaj D., Bolshakov S.,
RA Borodko D., Botchan M.R., Bruck D., Brodtier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davies P.,
RA de Pablo S.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C., Ferrari C., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey J., Helman T.J., Hernández J.R.J., Houck J.,
RA Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulpa D., Lai Z.,
RA Lasko P., Lei Y., Levitus A.A., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkliv G., Milashina N.V., Mobby C., Morris J., Mosherfi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Russkern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G.,
RA Reinert K., Rennington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson C., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stimpson M., Strong R., Sun E.,
RA Svartas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Westenbich J.,
RA Williams S.M., Woodward T., Weirley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2155-2195 (2000).
[2]

SEQUENCE OF 1-82 FROM N.A.
RN SEQUENCE OF 1-82 FROM N.A.
RN MEDLINE=95032110; PubMed=7945373;
RN Veensstra J.A.;
RT "Isolation and structure of the Drosophila corazonin gene.";
RN Blochem. Biophys. Res. Commun. 204:292-296 (1994).
[3]

SEQUENCE OF 20-30, AND AMTDATION.
RN SEQUENCE OF 20-30, AND AMTDATION.
RN TISSUE-Larva;
RN MEDLINE=95032110; PubMed=12171930;
RN Baggerman G., Christiaens A., De Loof A., Schoofs L.;
RT "Peptidomics of the larval Drosophila melanogaster central nervous
RT system";
RT RL J. Biol. Chem. 277:40368-40374 (2002);
CC |- FUNCTION: Cardiotoxic peptide. Corazonin is probably involved
CC in the physiological regulation of the heart beat.
CC |- SUBCELLULAR LOCATION: Secreted.

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CC ENBL; AB003704; AFAF55046_1; -.

DR EMBL: S74038; AAB312283_1; ALT_SEQ;
 DR FlyBase; FBgn0013777; Crz;
 KW Neuropeptide; Amidopeptide; Cleavage on pair of basic residues; Signal;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 19 CORAZONIN.
 FT PEPTIDE 20 30 CORAZONIN-PRECUSOR-RELATED PEPTIDE.
 FT PEPTIDE 34 67
 PROPEP 68 154 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 20 20 AMIDATION (G-11 PROVIDE AMIDE GROUP).
 FT MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
 FT CONFLICT 81 L -> Q (IN REF. 2).
 SQ SEQUENCE 154 AA; 17154 MW; 06046283A1C6TA2F CRC64;

Db 102 IAKSLLLP 109
 Search completed: March 1, 2004, 17:30:01
 Job time : 7 secs

RESULT 15
 YHJC_ECOLI STANDARD PRT; 299 AA.
 ID YHJC_ECOLI
 AC P37641;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Putative HTH-type transcriptional regulator yhJC.
 GN YHJC OR B3321.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID:562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=94316500; PubMed=8041620;
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
 region from 76.0 to 81.5 minutes.";
 RL Nucleic Acids Res. 22:2576-2586(1994).
 CC !- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.

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DR U0039; AAB1849_1; ALT_INIT.
 DR EMBL; AE000428; AAC76346_1; ALT_INIT.
 DR EcoGene; EG12247; Yhjc.
 DR InterPro; IPR00044; HTH_LysR.
 DR InterPro; IPR00519; LysR_subst.
 DR PFAM; PF00126; HTH_1.
 DR Pfam; PF03466; LysR_substrate_1.
 DR PROSITE; PS50931; HTH_LysR_1.
 KW Hypothetical Protein; Transcription regulation; DNA-binding;
 KW Complete proteome.
 FT DOMAIN 1 59 HTH_LYSR-TYPE.
 DNA BIND 19 38 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 299 AA; 33329 MW; 22D0E599C8C1 CRC64;
 Query Match 73.2%; Score 30; DB 1; Length 299;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARSLLLP 9 :|||||


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RESULTS 2
Qy   1 MARSLLPL 9
Db    1 MARSLLPL 9

RESULTS 2
Q9NZL1; PRELIMINARY; PRT; 396 AA.
ID Q9NZL1;
AC 01-OCT-2000 (TREMBLrel. 15; Created)
DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N_A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A.; Estivill X.; de La Luna S.; BACE2, is highly similar to
PT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
CYCogenet. Cell Genet. 89:177-184 (2000).
RL -1-. SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AF18977; RAP35836.1; -
DR HSSP; P00197; 2REN.
DR GO; GO:0004194; F:Pepsin A activity; IEA.
DR GO; GO:0008233; F:Peptidase activity; IEA.
DR GO; GO:0006508; P:Proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; AspartoProtease_AS.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR009001; Pept_A-Acid.
DR Pfam; PF00026; aspD; 1.
DR PRINTS; PR00732; PEPSEN.
DR PROSITE; PS00414; ASP_Protease; 2.
DR KW Aspartyl protease; Hydrolase; Protease.
SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match      85.4%; Score 35; DB 4; Length 396;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gap 0;
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RESULTS 3
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ID Q9NZL2;
AC 01-OCT-2000 (TREMBLrel. 15; Created)
DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE Aspartyl protease.
GN BACE2.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N_A.
RX MEDLINE=20422477; PubMed=10965118;
RA Solans A.; Estivill X.; de La Luna S.; BACE2, is highly similar to
PT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
RT Alzheimer's amyloid precursor protein beta-secretase.";
CYCogenet. Cell Genet. 89:177-184 (2000).
RL -1-. SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AF188216; AAF35635.1; -
DR HSSP; P00797; 2REN.
DR GO; GO:0004194; F:Pepsin A activity; IEA.
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DR	TIGR; CC0757; -;
GO	GO-0016021; C:integral to membrane; IEA.
DR	InterPro; IPR005495; YJGP_YJQ.
DR	InterPro; IPR005495; YJGP_YJQ.
PFam	PF03139; YJGP_YJQ.
KW	Hypothetical protein; Complete proteome.
SEQUENCE	397 AA; 42687 MW; AF05B915C02EDB8B CRC64;
SQ	
Query Match	Score 33; DB 10; Length 295;
Best Local Similarity	80.5%; Pred. No. 92;
Matches	0; Mismatches 0; Indels 0; Gaps 0;
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Ddb	18 MARSLLP 25
RESULT 12	
Q8SAT6	Preliminary; PRT; 368 AA.
ID	Q8SAT6
AC	Q8SAT6;
DT	01-JUN-2002 (TREMBLrel. 21, Created)
DT	01-OCT-2003 (TREMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Hypothetical protein.
OS	OSUNBA002D10.13
GN	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophytina; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC	Ehrhartoidae; Oryzeae; Oryza.
OX	NCBI_TaxID=4530;
RP	SEQUENCE FROM N.A.
RA	Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA	Sasaki C., Henry D., Oates R., Simmons J.,
RT	"Rice Genomic Sequence.";
RT	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RL	AC059402; AAL9349.1; -.
DR	Gramene; Q8SAT6; -.
KW	Hypothetical protein.
SEQUENCE	368 AA; 41064 MW; BD1BF772DA4F043F CRC64;
Query Match	Score 33; DB 10; Length 368;
Best Local Similarity	80.5%; Pred. No. 1.1e+02;
Matches	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MARSLLP 8
Ddb	18 MARSLLP 25
RESULT 13	
Q9AA49	Preliminary; PRT; 397 AA.
ID	Q9AA49
AC	Q9AA49;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Hypothetical protein CC0757.
GN	CC0757.
OS	Caulobacter crescentus.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC	Caulobacteraceae; Caulobacter.
OX	NCBI_TaxID=155899;
RN	SEQUENCE FROM N.A.
RP	STRAINATCC19099 / CB15/
RX	MEDLINE=21173698 / Published=11259647;
R2	Nierman W.C., Feilدبium T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smits J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback R., Tran K., Wolf A., Vamathevan J., Brinlalaeva M., White O., Salzberg S.L., Ventur J.C., Shapiro L., Fraser C.M.;
RT	"Complete genome sequence of Caulobacter crescentus.";
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR	EMBL; AAB22742.1; -.
PTR	BB7343; BB7343.
RESULT 14	
Q87F2	Preliminary; PRT; 424 AA.
ID	Q87F2
AC	Q87F2;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DB	Putative membrane transport protein.
GN	SAV6972.
OS	Streptomyces avermitilis.
OC	Bacteria; Actinobacterii; Actinomycetales; Streptomyces.
OC	Streptomyicinae; Streptomyctaceae; Streptomyces.
OX	[1] -
RN	[1] NCBI_TaxID=33903;
RP	SEQUENCE FROM N.A.
RC	STRAIN=VA-4580 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX	MEDLINE=21477403; Pubmed=11572948;
RA	Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA	Omura S., Ikeda H., Ishikawa J., Nakazawa H., Osone T.,
RA	Shinose M., Takahashi Y., Horikawa H., Hattori M.,
RA	Kiruchi H., Shiba T., Sakai Y., Hattori Y.,
RT	"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites";
RT	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=VA-4580 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX	MEDLINE=22603306; Pubmed=12692562;
RA	Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA	Sakai Y., Hattori M., Omura S.;
RT	"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
RL	Nat. Biotechnol. 21:526-531(2003).
DR	EMBL; AP005048; BAC74663.1; -.
KW	Complete proteome.
SQ	SEQUENCE 424 AA; 43493 MW; 500BA55A8D6BF80C CRC64;
Query Match	Score 33; DB 16; Length 424;
Best Local Similarity	80.5%; Pred. No. 1.3e+02;
Matches	7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Ddb	290 ARALLPL 297
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Q9ZRH9	Preliminary; PRT; 526 AA.
ID	Q9ZRH9
AC	Q9ZRH9;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Early embryogenesis protein.
GN	OSE351.
OS	Oryza sativa (Rice).
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza;
OC NCB_TAXID=4510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV; Tainung 67;
RA Tseng M.J.; Wang C.S.; Hsu H.R.;
RL Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U29968; ADD10369.1; -
DR Gramene; Q9ZRA9; -
DR GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR006044; Cupin.
DR InterPro; IPR006444; Sedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOULIN.
SQ SEQUENCE 526 AA; 58770 MN; BC23C019D1711F9B CRC84;
Query Match Score 33; DB 10; Length 526;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MARSILLPL 9
Db 6 MAASILLPL 14

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Job time : 32.3333 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:21:46 ; Search time 11.889 seconds
(without alignments)
39.081 Million cell updates/bec

Title: US-09-905-083-99
Perfect score: 42
Sequence: 1 QRIKAKSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

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3: /cgmn_6/pctdata/2/iaa/6A_COMB.pep:
4: /cgmn_6/pctdata/2/iaa/6B_COMB.pep:
5: /cgmn_6/pctdata/2/iaa/PCTUS_COMB.pep:
6: /cgmn_6/pctdata/2/iaa/backfile1.pop:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	42	100.0	9	3	US-09-502-600-99	Sequence 99, Appl
2	42	100.0	9	3	US-09-502-600-130	Sequence 99, Appl
3	42	100.0	9	4	US-09-918-243-99	Sequence 99, Appl
4	42	100.0	9	4	US-09-918-243-130	Sequence 99, Appl
5	42	100.0	144	4	US-09-618-259-4	Sequence 4, Appl
6	42	100.0	154	3	US-09-621-416-7	Sequence 7, Appl
7	42	100.0	224	3	US-08-914-483-33	Sequence 33, Appl
8	42	100.0	225	2	US-08-145-146-12	Sequence 12, Appl
9	42	100.0	225	2	US-09-027-337-4	Sequence 4, Appl
10	42	100.0	225	2	US-09-154-344-12	Sequence 12, Appl
11	42	100.0	225	4	US-09-644-600-4	Sequence 4, Appl
12	42	100.0	225	4	US-09-654-600-4	Sequence 4, Appl
13	42	100.0	253	2	US-08-557-146-2	Sequence 33, Appl
14	42	100.0	253	2	US-08-824-874-3	Sequence 3, Appl
15	42	100.0	253	2	US-09-154-344-2	Sequence 2, Appl
16	42	100.0	253	3	US-08-930-188-2	Sequence 2, Appl
17	42	100.0	253	3	US-09-210-084-3	Sequence 3, Appl
18	42	100.0	253	4	US-09-764-762-3	Sequence 3, Appl
19	42	100.0	253	5	PCT-US96-04294-2	Sequence 2, Appl
20	36	85.7	9	3	US-09-502-600-97	Sequence 97, Appl
21	36	85.7	9	4	US-09-918-243-97	Sequence 97, Appl
22	31	73.8	35	4	US-09-149-476-619	Sequence 619, Appl
23	31	73.8	250	1	US-07-914-282D-6	Sequence 6, Appl
24	31	73.8	250	1	US-08-276-887A-6	Sequence 6, Appl
25	31	73.8	250	2	PCT-US93-02460-6	Sequence 2, Appl
26	31	73.8	2860	2	US-08-826-267-2	Sequence 2, Appl
27	30	71.4	342	4	US-09-252-991A-18101	Sequence 18101, A

ALIGNMENTS

RESULT 1						
US-09-502-600-99	Sequence 99, Application US/09502600A					
	Patent No. 6294344					
	GENERAL INFORMATION:					
	APPLICANT: O'Brien, Timothy J.					
	TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer					
	FILE REFERENCE: D6223CIP-C					
	CURRENT FILING DATE: 2000-02-11					
	CURRENT APPLICATION NUMBER: US/09/502 600A					
	PRIOR APPLICATION NUMBER: 09/039,211					
	PRIOR FILING DATE: 03-14-1998					
	NUMBER OF SEQ ID NOS: 136					
	SEQ ID NO 99					
	LENGTH: 9					
	TYPE: PRT					
	ORGANISM: Homo sapiens					
	FEATURE:					
	OTHER INFORMATION: Residues 91-99 of the SCCE protein					
	US-09-502-600-99					

Query Match						
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Matches 9;	Conservative					
Qy	1 QRIKAKSKF 9					
Dy	1 QRIKAKSF 9					
RESULT 2						
US-09-502-600-130	Sequence 130, Application US/09502600A					
	Patent No. 6294344					
	GENERAL INFORMATION:					
	APPLICANT: O'Brien, Timothy J.					
	TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of Ovarian Cancer					
	FILE REFERENCE: D6223CIP-C					
	CURRENT FILING DATE: 2000-02-11					
	CURRENT APPLICATION NUMBER: US/09/502 600A					
	PRIOR APPLICATION NUMBER: 09/039,211					
	PRIOR FILING DATE: 03-14-1998					
	NUMBER OF SEQ ID NOS: 136					
	SEQ ID NO 130					
	LENGTH: 9					
	TYPE: PRT					
	ORGANISM: Homo sapiens					
	FEATURE:					

OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-502-600-130

Query Match Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 3
US-09-918-243-99
Sequence 99 Application US/09918243
Patent No. 6527403
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
CANNON, Martin J.
ASSIGNEE: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
PRIORITY FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 99
LENGTH: 9
TYPE: PRT
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-99

Query Match Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 4
US-09-518-243-130
Sequence 130 Application US/09918243
Patent No. 6527403
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
CANNON, Martin J.
ASSIGNEE: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
PRIORITY FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
SEQ ID NO 130
LENGTH: 9
TYPE: PRT
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-130

Query Match Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 5
US-09-618-259-4
Sequence 4 Application US/09618259
Patent No. 6542013
GENERAL INFORMATION:
APPLICANT: Underwood, Lowell J.
O'Brien, Timothy J.
TITLE OF INVENTION: No. 6542013el Extracellular Serine Protease
FILE REFERENCE: D602CIP2
CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
LENGTH: 144
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
US-09-618-259-4

Query Match Score 42; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 28 QRIKASKSF 36

RESULT 6
US-09-261-416-7
Sequence 7 Application US/09261416A
Patent No. 6291663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
Underwood, Lowell J.
TITLE OF INVENTION: TDG-12: A NO. 6291663el Transmembrane Serine Protease
FILE REFERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 154
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Overexpressed in Ovarian Carcinoma
US-09-261-416-7

Query Match Score 42; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 37 QRIKASKSF 45

RESULT 7
US-08-244-4^{a,3}
Sequence 5 Application US/08944483

Patent No. 6232456
 GENERAL INFORMATION:
 APPLICANT: COHEN, MAURICE L.
 APPLICANT: COLPITTS, TRACEY L.
 APPLICANT: FRIEDMAN, PAULIA N.
 APPLICANT: GRANADOS, EDWARD N.
 APPLICANT: KLASA, MICHAEL R.
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: STEWART, KENT D.
 APPLICANT: STROUPE, STEVEN D.
 TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
 AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
 TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
 TITLE OF INVENTION: OF THE PROSTATE
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/944,483
 FILING DATE: 12/04/2001
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6183.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935.1729
 TELEX: 847/938-2623
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 224 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6232456e
 US-08-944-483-33

Query Match 100.0%; Score 42; DB 3; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.24%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIKAASKSF 9
 Db 62 ORIKAASKSF 70

RESULT 8
 US-08-557-146-12
 Sequence 12, Application US/08557146
 ; Patent No. 5834290
 ; GENERAL INFORMATION
 ; APPLICANT: Egeland, Torbjorn
 ; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 ; TITLE OF INVENTION: Enzyme (SCCE)
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: White & Case, Patent Department
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York

Query Match 100.0%; Score 42; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.25%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIKAASKSF 9
 Db 63 ORIKAASKSF 71

RESULT 9
 US-09-027-337-4
 Sequence 4, Application US/09027337B
 ; Patent No. 5.972616
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; APPLICANT: Tanimoto, Hirotoshi
 ; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
 ; BREAST and Ovarian Carcinomas
 ; FILE REFERENCE: D6064
 ; CURRENT APPLICATION NUMBER: US/09/027,337B
 ; CURRENT FILING DATE: 1998-02-20
 ; NUMBER OF SEQ ID NOS: 13
 ; SEQ ID NO: 4
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Serine protease catalytic domain of Sccce homologous to
 ; TADG-15

Query Match 100.0%; Score 42; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.25%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIKAASKSF 9
 Db 63 ORIKAASKSF 71

RESULT 10
 US-09-154-344-12
 Sequence 12, Application US/09154344
 ; Patent No. 5981226
 ; GENERAL INFORMATION:

APPLICANT: Egelrud, Torbjorn
 APPLICANT: Hansson, Lennart Recombinant Stratum Corneum Chymotryptic
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case, Patent Department
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/154,344
 FILING DATE: 16-SEP-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sterner, Richard J.
 REGISTRATION NUMBER: 35,372
 REFERENCE/DOCKET NUMBER: 1103326-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 354-8113
 TELFAX: (212) 354-8113
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: polypeptide
 US-09-154-344-12

Query Match 100.0%; Score 42; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Number of SEQ ID NOS: 98

RESULT 13
 US-09-644-600-4
 Sequence 4, Application US/09644600
 GENERAL INFORMATION:
 Patent No. 6451500
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Tanimoto, Hirotoshi
 TITLE OF INVENTION: TAGC-15: An Extracellular Serine Protease
 TITLE OF INVENTION: Overexpressed in Carcinomas
 FILE REFERENCE: D6064CLP/D
 CURRENT APPLICATION NUMBER: US/09/644,600
 CURRENT FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: 09/421,213
 PRIOR FILING DATE: 1999-10-20
 PRIOR APPLICATION NUMBER: 09/027,337
 PRIOR FILING DATE: 1999-10-20
 NUMBER OF SEQ ID NOS: 98

Query Match 100.0%; Score 42; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Number of SEQ ID NOS: 98

RESULT 14
 US-09-654-600A-4
 Sequence 4, Application US/09654600A
 GENERAL INFORMATION:
 Patent No. 6549741
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Tanimoto, Hirotoshi
 TITLE OF INVENTION: TAGC-15: An Extracellular Serine Protease
 FILE REFERENCE: D6064CLP/D
 CURRENT APPLICATION NUMBER: US/09/654,600A
 CURRENT FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: 09/421,213
 PRIOR FILING DATE: 1999-10-20
 NUMBER OF SEQ ID NOS: 98

Query Match 100.0%; Score 42; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Number of SEQ ID NOS: 98

RESULT 15
 US-09-654-600A-4
 Sequence 4, Application US/09654600A
 GENERAL INFORMATION:
 Patent No. 6549741
 APPLICANT: O'Brien, Timothy J.
 APPLICANT: Tanimoto, Hirotoshi
 TITLE OF INVENTION: TAGC-15: An Extracellular Serine Protease
 FILE REFERENCE: D6064CLP/D
 CURRENT APPLICATION NUMBER: US/09/654,600A
 CURRENT FILING DATE: 1999-10-20
 PRIOR APPLICATION NUMBER: 09/421,213
 PRIOR FILING DATE: 1999-10-20
 NUMBER OF SEQ ID NOS: 98

Query Match 100.0%; Score 42; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Number of SEQ ID NOS: 98

RESULT 16
 US-09-557-146-2
 Sequence 2, Application US/09557146
 GENERAL INFORMATION:
 Patent No. 5834290
 APPLICANT: Egerrud, Torbjorn
 APPLICANT: Hansson, Lennart
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17
 NUMBER OF INVENTIONS: Enzyme (SCCE)
 CORRESPONDENCE ADDRESS:
 ADDRESS: White & Case, Patent Department
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2787
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION NUMBER: US/08/557,146
 CURRENT FILING DATE: 14-DEC-1995
 PRIOR APPLICATION NUMBER: US/08/557,146
 PRIOR FILING DATE: 1998-02-20
 NUMBER OF SEQ ID NOS: 98
 LENGTH: 225
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: SCCE

NAME: Steiner, Richard J.

REGISTRATION NUMBER: 35,372
 REFERENCE DOCKET NUMBER: 1103326-181
 TELEPHONE: (212) 819-8783
 FAX: (212) 354-8113
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-557-146-2

Query Match Score 42; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIASKSF 9
 Db 91 ORIASKSF 99

RESULT 14
 US-08-824-874-3
 Sequence 3, Application US/08824874
 Patent No. 5962300

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Insite Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 ZIP: 94304

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIAN TYPE: DOS
 OPERATING SYSTEM: DOS Compatible
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/824,874
 FILING DATE: Filed Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 FILING DATE:
 APPLICANT/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 LIBRARY: GenBank
 CLONE: 532504

US-08-824-874-3

Query Match Score 42; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIASKSF 9
 Db 91 ORIASKSF 99

Search completed: March 1, 2004, 17:38:27
 Job time : 12.8889 secs

RESULT 15
 US-09-154-344-2
 Sequence 2, Application US/09154344
 Patent No. 5981256

GENERAL INFORMATION:
 APPLICANT: Egelrud, Torbjorn
 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: White & Case, Patent Department
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2787

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/154,344
 FILING DATE: 16-SEP-1998
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/557,146
 FILING DATE: 14-DEC-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Stern, Richard J.
 REGISTRATION NUMBER: 35,372
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 354-8113
 TELEFAX: (212) 354-81783
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-154-344-2

Query Match Score 42; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIASKSF 9
 Db 91 ORIASKSF 99

Run on:	March 1, 2004, 17:16:55 ;	Search time	45.5556 Seconds
Perfect score:	42	(without alignments)	55.820 Million cell updates/sec
Title:	US-09-905-083-99		
Sequence:	1 ORIKASKSF 9		
Scoring table:	BLOSUM62		
Gapext:	10.0		
Searched:	1586107 seqs, 282547505 residues		
Total number of hits satisfying chosen parameters:	1586107		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	A_Geneseq_29Jan04:*		
	1: GeneseqP1900s:*		
	2: GeneseqP1990s:*		
	3: GeneseqP2000s:*		
	4: GeneseqP2001s:*		
	5: GeneseqP2002s:*		
	6: GeneseqP2003s:*		
	7: GeneseqP2003bs:*		
	8: GeneseqP2004s:*		
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.		
		SUMMARIES	
Result No.	Score	Query Match Length	DB ID Description
1	42	100.0	9 AAE08334 Human str
2	42	100.0	9 AAE08304 Human str
3	42	100.0	97 ADA05740 Human NOV
4	42	100.0	181 ADA05738 Human NOV
5	42	100.0	198 ADA05736 Human NOV
6	42	100.0	224 ADA05744 Human NOV
7	42	100.0	225 AAB98502 Human str
8	42	100.0	247 ADA05742 Human NOV
9	42	100.0	250 ADA05732 Human NOV
10	42	100.0	252 ADA05734 Human NOV
11	42	100.0	253 ADA05738 Human str
12	42	100.0	253 AAW55383 Human amy
13	42	100.0	253 ABB84421 Human SCC
14	42	100.0	253 ABB84406 Human SCC
15	42	100.0	253 AAU82740 Amino aci
16	42	100.0	253 Abu07440 Protein d
17	42	100.0	253 ABU07471 Human protein d
18	42	100.0	253 Abr5B471 Human str
19	42	100.0	253 ADB80484 Ovarian C
20	42	100.0	257 AAB21326 Human HSC
21	39	92.9	226 ABB84422 Rat SCC
22	37	88.1	136 ABG23378 Novel hum
23	36	85.7	9 AAE08302 Human str
24	36	85.7	11 ABBG8630 Stratum C
25	36	85.7	5 Abb84423 Murine SC
			ALIGNMENTS
			RESULT 1
			AAE08334 standard; peptide: 9 AA.
		XX	ID AAE08334;
		XX	AC AAE08334;
		XX	DT 01-NOV-2001 (first entry)
		XX	DB Human-stratum corneum chymotrypsin enzyme peptide #99 (residues 91-99).
		XX	KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
		XX	OS Homo sapiens.
		XX	PN WO20015158-A1.
		XX	PD 16-AUG-2001.
		XX	PP 07-FEB-2001; 2001WO-US003977.
		XX	PR 11-FEB-2000; 2000US-00502600.
		XX	PA (UYAR-) UNIV ARKANSAS.
		XX	PI Cibrien RJ;
		XX	DR WPI; 2001-514676/56.
		XX	PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
		XX	PS Disclosure; Page 124; 127pp; English.
		XX	CC The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide Sequence 9 AA.
		SQ Query Match	100.0%; Score 42; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ORIKASKSF 9
 Db 1 ||||| 1 ORIKASKSF 9

RESULT 2

AAE08304

ID AAE08304 standard; peptide; 9 AA.

XX

AC AAE08304;

XX

DT 01-NOV-2001 (first entry)

XX Human stratum corneum chymotrypsin enzyme peptide #69 (residues 91-99).
 DE XX Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.

XX Homo sapiens.

OS XX

PN WO200159158-A1.

XX

PD 16-AUG-2001.

XX

PP 07-FEB-2001; 2001WO-US003977.

XX

PR 11-FEB-2000; 2000US-00502600.

XX

DR WPI; 2001-514676/56.

XX

PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

XX

PS Claim 25; Page 117; 127pp; English.

XX

CC The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The present sequence is to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide.

XX Sequence 9 AA;

XX

Query Match Score 42; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIKASKSF 9Db 1 ||||| 1 ORIKASKSF 9

XX

PS RESULT 3

ADA05740

ID ADA05740 standard; protein; 97 AA.

XX

AC ADA05740;

XX

DT 06-NOV-2003 (first entry)

DE Human NOV18e protein SEQ ID NC:100.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; neuroprotective;
 KW anti-parkinsonian; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematoopoietic disorder; dyslipidaemia.
 XX Homo sapiens.

OS XX

PN WO2003029424-A2.

XX

ID 10-APR-2003.

XX

DT 02-OCT-2002; 2002WO-US031373.

XX

PR 02-OCT-2001; 2001US-0325483P.

DE PR 05-OCT-2001; 2001US-0327443P.

XX PR 05-OCT-2001; 2001US-032744P.

KW PR 09-OCT-2001; 2001US-0327917P.

KW PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

OS PR 09-OCT-2001; 2001US-032805P.

PN PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329114P.

PR PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330109P.

PD PR 22-OCT-2001; 2001US-034058P.

XX PR 24-OCT-2001; 2001US-0339266P.

PR PR 24-OCT-2001; 2001US-034362P.

XX PR 29-OCT-2001; 2001US-034557P.

PR PR 01-NOV-2001; 2001US-0344357P.

PA PR 17-APR-2002; 2002US-0372602P.

XX PR 19-APR-2002; 2002US-0373815P.

PI PR 19-APR-2002; 2002US-037817P.

XX PR 19-APR-2002; 2002US-0373826P.

PR PR 19-APR-2002; 2002US-0373844P.

XX PR 22-APR-2002; 2002US-0373844P.

PR PR 22-APR-2002; 2002US-037497P.

XX PR 16-MAY-2002; 2002US-038037P.

PT PR 16-MAY-2002; 2002US-038108P.

XX PR 16-MAY-2002; 2002US-0381042P.

PS PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

PR PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

PR PR 01-OCT-2002; 2002US-0392511.

XX PR 01-OCT-2002; 2002US-0392511.

XX XX (CURAGEN CORP.

PS Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PS Paturajan M, Spytek KA, Bainger SR, Elterman K, Mallyankar UM;

PS Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PS Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Sheroy SG;

PS Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PS WPI; 2003-381626/36.

PS DR N-PSDB; ADA0579.

XX

PT New NOVX polypeptides and nucleic acids useful for diagnosing,

PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,

PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX XX Claim 1; Page 171; 586pp; English.

XX XX

CC The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described is (1) a composition comprising a polypeptide

CC described above and a carrier; (2) a kit comprising, in one or more

CC containers, the composition described above; (3) an isolated nucleic acid

CC molecule which encodes a NOVX protein of the invention; (4) a vector

CC comprising the nucleic acid molecule described above; (5) a cell

CC comprising the above vector; (6) an antibody that immunospecifically

CC binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytotoxic, nootropic, neuroprotective, anticarsonian and antilipidaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

XX Sequence 97 AA;

Query Match Score 42; DB 6; Length 97;

Best Local Similarity 100.0%; Pred. No. 0.19%; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

AC ADA05738;

XX DT 06-NOV-2003 (first entry)

DE Human NOV18d protein SEQ ID NO:98.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytotoxic; nootropic; neuroprotective; anticarsonian; antilipidaemic; Gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. XX Homo sapiens.

XX WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0330142P. PR 05-OCT-2001; 2001US-0330399P. PR 05-OCT-2001; 2001US-0339262P. PR 24-OCT-2001; 2001US-0343699P. PR 24-OCT-2001; 2001US-0346152P. PR 01-NOV-2001; 2001US-0346352P. PR 17-APR-2002; 2002US-037320P. PR 19-APR-2002; 2002US-037385P. PR 19-APR-2002; 2002US-037386P. PR 19-APR-2002; 2002US-037384P. PR 22-APR-2002; 2002US-037977P. PR 16-MAY-2002; 2002US-038107P. PR 16-MAY-2002; 2002US-038108P. PR 16-MAY-2002; 2002US-038102P. PR 17-MAY-2002; 2002US-038365P. PR 28-MAY-2002; 2002US-038383P. PR 29-MAY-2002; 2002US-038381P. PR 25-JUN-2002; 2002US-039135P. PR 01-OCT-2002; 2002US-0026251I. XX PA (CURAGEN CORP.

XX PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Paturkar M, Spyke KA, Edinger SR, Ellerman K, Malanykar UN; Ort T, Gorman L, Zethsen BD, Anderson DW, Zhong M, Catterton E; PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergis C, Dippipo VA; PI Eisens AJ, Gangolli EA, Rieger DK, Spaderna SK; XX DR WPI: 2003-381626/36. N-2SDB; ADA05737.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidaemia, and in chromosome mapping, tissue typing or pharmacogenomics.

XX PS Claim 1; Page 171; 586PP; English.

XX CC The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with the polypeptide described above; (9) a polypeptide or nucleic acid molecule in a first mammalian subject; (10) a method for identifying an agent that binds to the polypeptide described above; (11) a method for producing the above polypeptide; (12) a method for modulating the activity or aberrant physiological interactions of the polypeptide; (13) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide described above; (14) a method for modulating the activity of the polypeptide described above; (15) a method for treating a pathology associated with the polypeptide described above; (16) a method for preventing a pathology associated with the polypeptide described above; (17) a method for producing the above polypeptide in a mammal; and (18) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytotoxic, nootropic, neuroprotective, anticarsonian and antilipidaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and

CC Pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

XX Sequence 181 AA;
SQ Query Match Score 42; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.36%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 72 QRIKASKSF 80

RESULT 5

ADA05736

ID ADA05736 standard; protein: 198 AA.

XX ADA05736;

AC DT 06-NOV-2003 (first entry)

XX Human NOV8c Protein SEQ ID NO:96.
DE ADA05736 standard; protein: 198 AA.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytosstatic; nootropic; neuroprotective;
KW immunoparkinsonian; antilipaemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX Homo sapiens.

OS WO2003029424-A2.

PN XX 10-APR-2003.

PD XX 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328099P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-DEC-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328494P.
PR 15-OCT-2001; 2001US-0329144P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330109P.
PR 24-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 29-OCT-2001; 2001US-0343829P.
PR 01-NOV-2001; 2001US-0349515P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373847P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381632P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383331P.
PR 01-OCT-2002; 2002US-0391335P.
XX PA (CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI PA human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Mallyankar UM;
Ort T, Gorman L, Zernusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangoli EA, Rieger DK, Spaderna SK;
XX DR WPI: 2003-381626/36.
XX DR N-PSDB; ADA05735.
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PR preventing or treating NOVX-associated disorders, e.g., diabetes, obesity,
PR cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PR pharmacogenomics.
XX PS Claim 1; Page 170; 586pp; English.
XX CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent. For
use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide described above; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytosstatic, nootropic, neuroprotective, antiparkinsonian
CC and analgesic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haemato poetic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

XX SQ Sequence 198 AA;

Query Match Score 42; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.39%; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; 1 QRIKASKSF 9
QY 91 QRIKASKSF 99
Db

RESULT 6

ADA05744

ID XX

AC XX

ADA05744;

DT DT

06-NOV-2003 (first entry)

XX DB Human NOV1g protein SEQ ID NO:104.

KW XX

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; anilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX OS Homo sapiens.
 XX WO2003029424-A2.
 PN 10-APR-2003.
 XX 02-OCT-2002; 2002WO-US031373.
 PF 02-OCT-2001; 2001US-032648P.
 PR 02-OCT-2001; 2001US-032745P.
 PR 05-OCT-2001; 2001US-032744P.
 PR 09-OCT-2001; 2001US-032791P.
 PR 09-OCT-2001; 2001US-032803P.
 PR 09-OCT-2001; 2001US-032804P.
 PR 09-OCT-2001; 2001US-032805P.
 PR 12-OCT-2001; 2001US-032884P.
 PR 15-OCT-2001; 2001US-032941P.
 PR 17-OCT-2001; 2001US-033014P.
 PR 18-OCT-2001; 2001US-033030P.
 PR 22-OCT-2001; 2001US-034105P.
 PR 24-OCT-2001; 2001US-033926P.
 PR 24-OCT-2001; 2001US-034362P.
 PR 29-OCT-2001; 2001US-034957P.
 PR 01-NOV-2001; 2001US-034635P.
 PR 17-APR-2002; 2002US-037326P.
 PR 19-APR-2002; 2002US-037381P.
 PR 19-APR-2002; 2002US-037382P.
 PR 19-APR-2002; 2002US-037384P.
 PR 22-APR-2002; 2002US-037497P.
 PR 16-MAY-2002; 2002US-037382P.
 PR 16-MAY-2002; 2002US-038103P.
 PR 16-MAY-2002; 2002US-038104P.
 PR 17-MAY-2002; 2002US-038164P.
 PR 28-MAY-2002; 2002US-038365P.
 PR 29-MAY-2002; 2002US-038383P.
 PR 01-OCT-2002; 2002US-0391335P.
 XX (CURA-) CURAGEN CORP.
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Sptreka KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zethusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee MD, Berghs C, DiPippo VA;
 PI Eisen AU, Ganguli EA, Rieger DK, Spaderna SK;
 DR WPI; 2003-381626/36.
 DR N-PSDB; ADA05743.

XX New NOX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Claim 1; Page 172; 586pp; English.

XX The present invention describes NOX proteins, where X can be 1 to 55 (e.g. NO1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell binds to the polypeptide described above; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a

CC sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating a or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipidemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haemopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOX from the present invention.

CC Sequence 224 AA;

CC SQ Query Match 100.0%; Score 42; DB 6; Length 224;
 CC Best Local Similarity 100.0%; Pred. No. 0.45;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 ORITAKSKSF 9
 CC Db 77 QRTAKSKSP 85

RESULT 7

CC ID AAB98502 standard; protein; 225 AA.
 XX ID AAB98502 standard; protein; 225 AA.
 XX ID AAB98502 standard; protein; 225 AA.
 XX AC AAB98502;
 XX AC AAB98502;
 XX DT 03-APR-2001 (first entry)
 DE Human Stratum Corneum Chymotryptic Enzyme SCCE, catalytic domain.
 XX Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
 KW tumour antigen-derived gene 15; serine protease;
 KW Stratum Corneum Chymotryptic Enzyme; SCCE.
 XX Homo sapiens.
 XX OS Homo sapiens.
 XX PN WO200129056-A1.
 XX PD 26-APR-2001.
 XX PD 26-APR-2001.
 XX PD 26-APR-2001.
 XX PR 20-OCT-2000; 20000NO-US029095.
 XX PR 20-OCT-1999; 99US-00421213.
 XX PA (UYAR-) UNIV ARKANSAS.
 XX PA O'brien TJ, Tanimoto H;
 XX PI O'brien TJ, Tanimoto H;
 XX DR WPI; 2001-381031/40.
 XX PT Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
 XX PS Example 10; Fig 1; 130pp; English.

PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0341926P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0344957P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381622P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391315P.
 PR 01-OCT-2002; 2002US-0026251I.
 XX (CURA-) CURAGEN CORP.
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, DE
 PI Patterson M, Spytek KA, Edinger SR, Elleman K, Malyakkar UM, XX
 PI Ort T, Corman L, Zerhusen BD, Anderson DW, Zhong M, Cotterton B; KW
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; KW
 PI Shimkets RA, Rosenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; KW
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; KW
 XX DR; ADA5733, N-PSDB; ADA5733, DR
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing, PT
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, PR
 cancer or dyslipidemia, and in chromosome mapping, tissue typing or PR
 pharmacogenomics. XX
 XX Claim 1; Page 170; 586pp; English.
 XX The present invention describes NOVX proteins, where X can be 1 to 55 CC
 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide CC
 described above and a carrier; (2) a kit comprising, in one or more CC
 containers, the composition described above; (3) an isolated nucleic acid CC
 molecule which encodes a NOVX protein of the invention; (4) a vector CC
 comprising the nucleic acid molecule described above; (5) a cell CC
 comprising the above vector; (6) an antibody that immunospecifically CC
 binds to the polypeptide described above; (7) methods for determining the CC
 presence or amount of the above polypeptide or nucleic acid molecule in a CC
 sample; (8) methods for determining the presence of or predisposition to CC
 a disease associated with altered levels of expression of the above CC
 polypeptide or nucleic acid molecule in a first mammalian subject; (9) a CC
 method of identifying an agent that binds to the polypeptide described CC
 above; (10) a method for identifying potential therapeutic agent for CC
 use in treating a pathology that is related to an aberrant expression or CC
 aberrant physiological interactions of the polypeptide; (11) a method of CC
 screening for a modulator of activity or of latency or predisposition to CC
 a pathology associated with the polypeptide; (12) a method for modulating CC
 the activity of the polypeptide described above; (13) methods of treating CC
 or preventing a pathology associated with the above polypeptide in a CC
 mammal; and (14) method for producing the above polypeptide. NOVX CC
 sequences have antiobtacitic, anorectic, antiparkinsonian, CC
 immunomodulator, cytostatic, neuroprotective, anticancer, CC
 and antiinflammatory activities, and can be used in gene therapy. The CC
 polypeptide is useful in manufacturing a medicament for treating a CC
 syndrome associated with a human disease. The polypeptide or the nucleic CC
 acid molecule may be used to diagnose, treat or prevent metabolic CC
 disorders such as diabetes or obesity, infections, cachexia, cancer, CC
 neurodegenerative disorders such as Alzheimer's disease or Parkinson's CC
 disease, immune disorders, haematopoietic disorders and various CC
 dyslipidaemias. The nucleic acids can also be used as hybridisation CC
 probes, in chromosome mapping, tissue typing, preventive medicine and CC
 pharmacogenomics. The present sequence represents a human NOVX from the CC
 present invention.
 XX SQ Sequence 252 AA;
 Query Match Score 42; DB 6; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QRIKASKSF 9
 DB 90 QRIKASKSF 98
 RESULT 11
 AAM67888 ID AAR67888 standard; protein; 253 AA.
 XX AC AAR67888;
 XX DT 25-MAR-2003 (revised)
 DT 09-AUG-1995 (first entry)
 XX DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
 XX XX
 XX Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
 XX callosities; keratosis pilaris; ichthyoses; eczema.
 XX Homo sapiens.
 XX OS HO9500651-A1.
 XX PN 05-JAN-1995.
 XX PD 20-JUN-1994;
 XX PP 94WO-TB00066.
 XX PR 18-JUN-1993;
 XX PR 93DK-00000725.
 PA (SYMB-) SYMBICOM AB.
 XX PA
 XX Egelrud T, Hansson L;
 XX PI
 XX DR WPI; 1995-05208B/07.
 DR N-PSDB; AAQ81203.
 XX PT
 PT PR Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and PR
 PR related vectors, transformed cells and polypeptides, useful for treating PR
 PR skin disorders, e.g. acne or psoriasis, and for identification of PR
 PR specific inhibitors.
 PR Disclosure; Page 97; 137pp; English.
 XX CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic CC
 CC and skin care products, especially to treat and prevent acne, xerosis, CC
 CC or other hyperkeratotic conditions (e.g. callousness or keratosis CC
 CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced CC
 CC recombinantly following mammal, insect, plant, or microorganism CC
 CC transformation with plasmid pSS07. (Updated on 25-MAR-2003 to correct PN CC
 CC field.)
 XX SQ Sequence 253 AA;
 Query Match Score 42; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QRIKASKSF 9

RESULT 12	
Db	91 QRIKASKSF 99
ID	AAW05383
VID	AAW05383 Standard; protein; 253 AA.
XX	
AC	AAW05383;
XX	
CC	31-DEC-1996 (first entry)
DDT	Human amyloid precursor protein protease.
XX	
DE	Amyloid precursor protein protease; Alzheimer's disease; diagnosis; therapy.
XX	
KW	
KW	Homo sapiens.
OS	
XX	
PN	WO9631122-A1.
XX	
PPD	10-OCT-1996.
XX	
PPF	02-APR-1996; 96WO-US004294.
XX	
PR	04-APR-1995; 95US-00416257.
XX	
PA	(ELIL) LILLY & CO ELLI.
XX	
PI	Dixon EP, Johnstone EM, Little SP;
XX	
PT	WPI; 1996-4664/46.
DR	N-PSDB; AT39753.
XX	
PT	New isolated human amyloid precursor protein protease - used to develop products for the treatment or diagnosis of associated conditions, esp; Alzheimer's disease.
PT	
XX	
PS	Claim 1; Page 44-45; 55pp; English.
XX	
CC	Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39753) obtained from a human lung library. Recombinant protease can be produced transformed or transfected prokaryotic (bacterial, E. coli) or eukaryotic (yeast, Pichia pastoris, CHO, HEK293T) host cells. It is used to develop products for the diagnosis and testing of cpd's associated with beta-amyloid peptide, esp. Alzheimer's disease.
CC	
CC	Sequence 253 AA;
CC	
CC	Query Match Score 42; DB 2; Length 253;
CC	Best Local Similarity 100.0%; Pred. No. 0.51;
CC	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 QRIKASKSF 9
DB	91 QRIKASKSF 99
RESULT 13	
ID	ABB84421
VID	ABB84421 standard; peptide; 253 AA.
AC	ABB84421;
XX	
CC	08-NOV-2002 (first entry)
CC	Human SCCE protein N-terminal fragment SEQ ID 4B.
XX	
CC	SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX	

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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:35:01 ; search time 24.1111 seconds
(without alignments)
78.818 Million cell updates/sec

Title: US-09-905-083-99
Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 809742 sqs, 211153259 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Published_Applications_AA:**

1: /cgn2_6/prodata/1/pubpa/us07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpa/us06_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpa/us05_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubpa/us04_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpa/us07_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubpa/PCUT_PUBCOMB.pep:*

7: /cgn2_6/prodata/1/pubpa/us08_NEW_PUB.pep:*

8: /cgn2_6/prodata/1/pubpa/us09_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubpa/us09_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubpa/us09_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubpa/us09_PUBCOMB.pep:*

12: /cgn2_6/prodata/1/pubpa/us09_NEW_PUB.pep:*

13: /cgn2_6/prodata/1/pubpa/us10_PUBCOMB.pep:*

14: /cgn2_6/prodata/1/pubpa/us10_PUBCOMB.pep:*

15: /cgn2_6/prodata/1/pubpa/us10_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpa/us60_NEW_PUB.pep:*

17: /cgn2_6/prodata/1/pubpa/us60_NEW_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpa/us60_PUBCOMB.pep:*

16 78.6 427 1.4 US-10-005-956-574
17 78.6 427 1.4 US-10-005-956-576
18 78.6 427 1.4 US-10-005-956-578
19 78.6 427 1.4 US-10-005-956-583
20 78.6 427 1.4 US-10-005-956-855
21 73.8 3.5 10 US-09-809-391-119
22 73.8 3.5 10 US-09-882-171-619
23 73.8 276 15 US-10-108-160A-3762
24 73.8 298 15 US-10-168-659-20
25 73.8 319 15 US-10-369-493-209
26 73.8 1201 10 US-09-863-776-61
27 73.8 2861 15 US-10-374-979-108
28 73.8 2861 15 US-10-331-496A-89
29 73.8 3038 10 US-10-369-493-18492
30 71.4 627 15 US-10-369-493-18492
31 29 69.0 46 10 US-09-764-891-753
32 29 69.0 127 14 US-10-971-111-333
33 29 69.0 187 13 US-10-062-554-168
34 29 69.0 200 13 US-10-062-254-170
35 29 69.0 205 13 US-10-062-254-170
36 29 69.0 206 13 US-10-062-554-128
37 29 69.0 438 10 US-09-769-736-137
38 28 66.7 61 9 US-09-912-020-357
39 28 66.7 84 9 US-09-864-761-42601
40 28 66.7 95 9 US-09-867-510-1226
41 28 66.7 240 11 US-09-833-445-884
42 28 66.7 265 15 US-10-374-780A-1929
43 28 66.7 306 15 US-10-369-493-1389
44 28 66.7 374 15 US-10-369-493-11176
45 28 66.7 416 15 US-10-369-493-1521

ALIGNMENTS

RESULT 1
US-09-918-243-99

; Sequence 99, Application US/09918243

; General Information: O'Brien, Timothy J.

; Applicant: Cannon, Martin J.

; Applicant: Santini, Alessandro

; Title of Invention: Methods for the early diagnosis of ovarian cancer

; Current Application Number: D6232CIP/C/DCIP

; File Reference: D6232CIP/C/DCIP

; Current Filing Date: 2001-07-30

; Prior Application Number: US/09/918-243

; Prior Filing Date: 2001-07-13

; Number of Seq ID NOS: 136

; SEQ ID NO 99

; LENGTH: 9

; TYPE: PRT

; Feature:

; Name Key: CHAIN

; Other Information: Residues 91-99 of the SCCE protein
US-09-918-243-99

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	42	100.0	9	US-09-918-243-99
2	42	100.0	9	US-09-918-243-130
3	42	100.0	9	US-09-905-083-99
4	42	100.0	9	US-09-905-083-130
5	42	100.0	144	US-10-796-294-4
6	42	100.0	144	US-10-161-78-4
7	42	100.0	253	US-09-888-615-98
8	42	100.0	253	US-09-784-762-3
9	42	100.0	253	US-10-264-233-90
10	42	100.0	253	US-10-235-021-498
11	42	100.0	253	US-10-173-991-48
12	36	85.7	9	US-09-918-243-97
13	36	85.7	9	US-09-905-083-97
14	33	78.6	427	US-10-180-4
15	33	78.6	427	US-10-005-956-572

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match Score 42; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 9; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ORIKASKSF 9
Db 1 ORIKASKSF 9

RESULT 2
US-09-918-243-130

; Sequence 13, Application US/09918243
; Patent No. US/000142317A1

; General Information:

NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; US-10-461-787-4
Query Match Score 42; DB 14; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.44%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ORIKAASKF 9
Db 28 ORIKAASKF 36

RESULT 7
US-09-888-615-98
Sequence 98, Application US/09888615
Patent No. US2002006485A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEL, SEAN
APPLICANT: CHARYDCZAK, GILEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 0186 02/1214
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 98
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-615-98

Query Match Score 42; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.77%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ORIKAASKF 9
Db 91 ORIKAASKF 99

RESULT 8
US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. US2002006834A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: PF-0252 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match Score 42; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.77%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ORIKAASKF 9
Db 91 ORIKAASKF 99

RESULT 9
US-10-264-283-90
Sequence 90, Application US/10264283
Publication No. US2003014449A1
GENERAL INFORMATION:
APPLICANT: Aligat, Paul A.
APPLICANT: Manning, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121-590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Corixa Disclosure Database
SEQ ID NO: 90
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-283-90

RESULT 10
US-10-295-027-498
Sequence 498, Application US/10295027
Publication No. US2003023235A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard

Db 2 QRIKASKS 9

RESULT 14
 US-09-993-180-4
 Sequence 4; Application US/09993180
 Publication No. US2003005445A1
 GENERAL INFORMATION:
 APPLICANT: BRISTOL-MYERS SQUIBB Company
 TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM LYMPHO
 FILE REFERENCE: D0051.NP
 CURRENT APPLICATION NUMBER: US/09/993,180
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: US 60/248,434
 PRIOR FILING DATE: 2000-11-14
 PRIOR APPLICATION NUMBER: US 60/257,610
 PRIOR FILING DATE: 2000-12-21
 PRIOR APPLICATION NUMBER: US 60/282,745
 PRIOR FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 4
 LENGTH: 427
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-993-180-4

Query Match: 78.6%; Score 33; DB 10; Length 427;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKS 9
 Db 355 QKLEASKSF 363

RESULT 15
 US-10-005-956-572
 Sequence 572; Application US/10005956
 Publication No. US20030113726A1
 GENERAL INFORMATION:
 APPLICANT: BRISTOL-MYERS SQUIBB Company
 TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 FILE REFERENCE: D0053NP
 CURRENT APPLICATION NUMBER: US/10/005,956
 CURRENT FILING DATE: 2001-12-03
 PRIOR APPLICATION NUMBER: 60/251,015
 PRIOR FILING DATE: 2000-12-04
 PRIOR APPLICATION NUMBER: 60/263,578
 PRIOR FILING DATE: 2001-01-23
 PRIOR APPLICATION NUMBER: 60/273,037
 PRIOR FILING DATE: 2001-03-02
 NUMBER OF SEQ ID NOS: 1579
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 572
 LENGTH: 427
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-005-956-572

Query Match: 78.6%; Score 33; DB 14; Length 427;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKS 9
 Db 355 QKLEASKSF 363

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:21:01 ; Search time 10.2222 Seconds
 (without alignments)

Title: US-09-905-083-99
 Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : PIR_78:
 1: Pir1:
 2: Pir2:
 3: Pir3:
 4: Pir4:
 *
 *
 *
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	253	A53768	serine protease serine proteinase protein T24A6.11 [
2	34	81.0	373	D89004	kallistatin precursor probable DNA-directed tetrachloro-p-hydroxy-beta-SNAP protein
3	33	78.6	427	A49518	beta-SNAP protein
4	32	76.2	895	D72571	maki-like protein
5	31	73.8	248	A40525	BET1 protein - yeast
6	31	73.8	298	S32368	probable phosphatase
7	31	73.8	302	T50147	probable endopeptidase P-loop ATPase
8	31	73.8	362	F81409	probable dehydrogenase
9	30	71.4	142	C3810	hypothetical protein
10	30	71.4	321	C71163	hypothetical protein
11	30	71.4	331	H97051	hypothetical protein
12	30	71.4	427	T48159	hypothetical protein
13	30	71.4	517	T40129	neutral endopeptidase
14	30	71.4	627	C86850	lactococcal endopeptidase Fepo
15	30	71.4	627	A47098	hypothetical protein
16	30	71.4	627	F53290	pyruvate dehydrogenase
17	30	71.4	675	T19678	hypothetical protein
18	30	71.4	985	D82776	probable ubiquitin
19	30	71.4	1102	H84545	dystrophin, muscle
20	30	71.4	3660	S02441	hypothetical protein
21	29	69.0	65	AF2269	16K protein - toba
22	29	69.0	141	B43322	NADH dehydrogenase
23	29	69.0	172	H81251	hypothetical protein
24	29	69.0	182	C64176	thiogalactoside acyltransferase
25	29	69.0	203	C906778	quinoinate phosphotriesterase
26	29	69.0	203	G85528	WD repeat protein
27	29	69.0	268	E84339	similarity to C4-type zinc fingers
28	29	69.0	349	AE2368	C;Genetics:
29	29	69.0	368	T225587	A;Gene: T24A6.11

ALIGNMENTS

RESULT 1

A53768

serine Proteinase SCCE precursor - human
 N;Alternate names: stratum corneum chymotryptic enzyme

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999

C;Accession: A53768

R;Hansson, L.; Stroemqvist, M.; Baecman, A.; Wallbrandt, P.; Carlstein, A.; Egeirrud, T.

J. Biol. Chem. 269, 19420-19426, 1994

A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym

A;Reference number: A53968; PMID:8038225; PMID:8034709

A;Accession: A53968

A;Status: Preliminary

A;Molecule type: mRNA

A;Residue: 1-253 <HAN>

A;Cross-references: GB:L33404; NID:9521214; PID: AAC37551.1; PID:9532504

C;Genetics:

A;Gene: GDB:PRSS6; SCCE

A;Cross-references: GDB:377730

A;Map position: 7q35-7q35

C;SuperFamily: trypsin homology <TRY>

F;30-245/Domain: trypsin homology

Query Match

100.0%

Score: 42;

DB 2;

Length: 253;

Best Local Similarity

100.0%;

Matches

9;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

QRIKASKSF

9

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R;Anonymous, The C. elegans Sequencing Consortium.

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C;Accession: D89004

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A;Reference number: A50000; MUR:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_eleg

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and R;Anonymous, The C. elegans Sequencing Consortium.

A;Accession: D89004

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology

A;Reference number: A50000; MUR:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_eleg

A;Accession: D89004

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-373 <STO>

A;Cross-references: GB:chrV; PID: AAC17798.1; PID:93168946; GSPDB:GN00023; CESP:T24A6.1

A;Note: contains similarity to C4-type zinc fingers

C;Genetics:

A;Gene: T24A6.11

RESULTS 7

50147 Mak16-like protein [Imported] - fission yeast (Schizosaccharomyces pombe)
 Species: Schizosaccharomyces pombe
 Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 Accession: TS0147
 Submitted to the EMBL Data Library, November, 1999
 Reference number: 225043
 Status: preliminary; translated from GB/EMBL/DDJB
 Cross-references: EMBL:AL132798; PIDN:CAB60698_1; GSPDB:GN00066; SPDB:SPAC222.06
 Residues: 1-102 <PRT>
 Experimental source: strain 972h(-); cosmid c222
 Gene: SPDB:SPAC222.06
 Genetics:
 Molecule type: DNA
 Map Position: 1
 Introns: 21/2
 Superfamily: MAK16 protein

Query Match Score 31; DB 2; Length 302;
 Best Local Similarity 73.8%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ORIASKSF 9
 Db 78 QRIKALKY 86

RESULTS 8

81409 phosphate transporter system permease protein Cj0615 [Imported] - Campylobacter jejuni
 Species: Campylobacter jejuni
 Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 Accession: F81409
 Parthiban, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, T.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanTieghem, A.; Whitehead, S.; Barrell, G.B.; Project: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypotheses for its pathogenicity
 Reference number: A81250; PMID:20150912; PMID:10688204
 Genetics:
 Molecule type: DNA
 Residues: 1-362 <PRT>
 Experimental source: serotype O2, strain NCTC 11168
 Gene: psba; Cj0615

Query Match Score 31; DB 2; Length 362;
 Best Local Similarity 73.8%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ORIASKSF 9
 Db 7 KRQKASKSF 15

RESULTS 9

339610 BET1 protein - yeast (Saccharomyces cerevisiae)
 Alternative names: Protein YIA1; Protein YIL004C; SLY12 protein
 Species: Saccharomyces cerevisiae
 Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 29-Oct-1999
 Dasscher, C.; Osig, R.; Galwitz, D.; Schmitt, H.D.
 Mol. Cell. Biol. 11, 872-885, 1991
 Genetics: Identification and structure of four yeast genes (SLY1) that are able to suppress
 R.Rowley, N.

Submitted to the EMBL Data Library, August 1994

Reference number: A39610; MUID:9117254; PMID:1990290

A;Accession: C39610
 A;Molecule type: DNA
 A;Residues: 1-142 <DAS>
 A;Cross-references: ENBL:X54237; NID:94483; PIDN:CAA3814

A;Reference number: A39610
 A;Accession: S48442
 A;Accession: S48453
 A;Molecule type: DNA
 A;Residues: 1-142 <ROW>
 A;Cross-references: GB:Z47047; EMBL:Z38113; NID:g603997
 Rios, H.; Tamames, J.; Tedoro, C.; Valencia, A.; Sena, M.; Yeast 11, 61-78, 1995
 A;Title: Nucleotide sequence and analysis of the centromeric region of chromosome 11 of *Saccharomyces cerevisiae*
 A;Reference number: S50795; MUID:9528251; PMID:7762303
 A;Accession: S58677
 A;Status: nucleic acid sequence not shown; translation not available
 A;Molecule type: DNA
 A;Residues: 1-142 <VOVS>
 A;Cross-references: ENBL:X79743
 A;Not: the nucleotide sequence was submitted to the EMBL Data Library
 C;Genetics:
 A;Gene: SGD:BET1; SLY12
 A;Cross-references: SGD:SG0001266; MIPS:YIL004C
 A;Map position: 9L
 A;Introns: 4/2
 C;Keywords: transmembrane protein
 F:126-142/Domain: transmembrane #status predicted <TM>
 Query Match Score 71.4%; Pred. No. 26;
 Best Local Similarity 87.5%; Conservative 7; Mismatches 0;
 Matches 1; I

QY 1 ORIASKSF 8
 Db 67 QRIKALKY 74

RESULTS 10

C71463 probable p-loop ATPase - *Chlamydia trachomatis* (serotype L2)
 Species: *Chlamydia trachomatis*
 C;Accession: C71463
 R;Stephans, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marin, M.; Science 282, 754-759, 1998
 A;Title: Genome sequence of an obligate intracellular pathogen of humans
 A;Reference number: A71570; MUID:99000809; PMID:9784136
 A;Accession: C71463
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-321 <ARN>
 A;Cross-references: GB:AB001357; GB:AE001273; NID:933298
 A;Experimental source: serotype D, strain UW-3/Cx
 C;Genetics:
 A;Gene: mesU

Query Match Score 71.4%; Pred. No. 60;
 Best Local Similarity 66.7%; Conservative 6; Mismatches 2;
 Matches 1; I

QY 1 ORIASKSF 9
 Db 277 ERIVASKSF 285

RESULTS 11

H97051 probable dehydrogenase, YIL004B, *subtilis ortholog* [impo
 C;Species: *Clostridium acetobutylicum*
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C;Accession: H97051

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.						
I protein - protein search, using SW model						
Run on:		March 1, 2004, 17:17:25 ; Search time 6 Seconds (without alignments)		78.105 Million cell updates/sec		
title:	US-09-905-083-99	maximum DB seq length:	0			
perfect score:	42	maximum DB seq length:	2000000000			
sequence:	1 QRIKASKSF 9					
scoring table:	BLOSUM62					
gapopen:	10.0	Gapext:	0.5			
searched:	141681 seqs, 52070155 residues	total number of hits satisfying chosen parameters:	141681			
database:	SwissProt_42:*	total number of hits satisfying chosen parameters:	141681			
post-processing:	Minimum Match 0%	Maximum Match 100%				
	Listing first 45 summaries					
		SUMMARIES				
result No.	Score	Query	Match Length	DB ID	Description	
1	42	100.0	253	1 KLK7_HUMAN	P49962 homo sapiens	
2	34	81.0	107	1 YI97_PASMU	Q9cj49 pasteurella	
3	33	78.6	314	1 RLA0_THEAC	P26692 thermoplasma	
4	33	78.6	427	1 KAIN_HUMAN	P29652 homo sapiens	
5	32	76.2	161	1 RL10_MCP6	Q8evj0 mycoplasma	
6	7	31	73.8	247	P05320 spinigobius	
7	31	73.8	298	1 SNAB_BOVIN	P81126 bos taurus	
8	31	73.8	298	1 SNAB_HUMAN	Q9h115 homo sapiens	
9	31	73.8	3038	1 TRIO_HUMAN	Q75962 mus musculus	
10	30	71.4	142	1 BET1_YEAST	P22804 saccharomyces	
11	30	71.4	517	1 YB3C_SCOPHO	O14342 schizosaccharomyces	
12	30	71.4	626	1 PEPO_LACLCA	Q07744 lactococcus	
13	30	71.4	621	1 PEPO_LACLC	O09145 lactococcus	
14	30	71.4	727	1 PKP1_BOVIN	Q28161 bos taurus	
15	30	71.4	728	1 PKP1_MOUSE	P97577 gallus gallus	
16	30	71.4	747	1 PKP1_HUMAN	Q13835 homo sapiens	
17	30	71.4	3660	1 DMD_CHICK	P11533 tobacco mosaic virus	
18	29	69.0	141	1 V16_K_TRVPL	P45340 haemophilus	
19	29	69.0	182	1 ORN_HABIN	Q7vra0 haemophilus	
20	29	69.0	336	1 GDP4A_HAEVDU	Q97856 clostridium	
21	29	69.0	463	1 SYN_CLOIDIUM	P70765 actinobacteria	
22	29	69.0	484	1 GPGD_ACTAC	P31803 escherichia coli	
23	29	69.0	598	1 CALI_HUMAN	Q13939 homo sapiens	
24	29	69.0	738	1 CNG7_ARATH	Q8bzr9 photobacteris	
25	29	69.0	761	1 YKC2_CAEEL	P41993 caenorhabditis	
26	29	69.0	853	1 DIA3_HUMAN	Q9nsv4 homo sapiens	
27	28	65.7	46	1 DIH9_HUMAN	P23465 locusta migratoria	
28	28	65.7	61	1 CSRA_ECOLI	Q47620 erwinia carotovora	
29	28	66.7	61	1 CSRA_ERWCA	Q85735 serratia marcescens	
30	28	66.7	61	1 CSRA_PHOLI	Q89791 bifidobacterium	
31	28	66.7	69	1 CSRA_SERMA	PR01240 bacillus	
32	28	66.7	63	1 CPRO_BACSU		

RESULT 1		ALIGNMENTS	
KLK7_HUMAN	STANDARD;	PRT;	253 AA.
ID : KLK7_HUMAN			
AC : P49622;			
DT : 01-OCT-1996	(Rel. 34, Created)		
DT : 01-OCT-1996	(Rel. 34, Last sequence update)		
DT : 10-OCT-2003	(Rel. 42, Last annotation update)		
DE : Kalikrein 7 Precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (HSCCE).			
DE : KLK7 OR PRSS6 OR SCCE.			
GN : Homo sapiens (Human).			
OS : Homo sapiens (Human).			
OC : Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OC : Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX : NCBI_TAXID=9606;			
RN : [1]	SEQUENCE FROM N.A., AND SEQUENCE OF 23-53.		
RC : TISSUE=Skin;			
RX : MEDLINE=94308225; PubMed=8034709;			
RA : Hansson L., Stroemqvist M., Baekman A., Wallbrandt P., Carlstein A., Egeirud T.;			
RA : "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";			
RT : J. Biol. Chem. 269:19420-19426(1994).			
RL : [2]	SEQUENCE FROM N.A.		
RP : TISSUE=Keratinocytes;			
RC : Yousef G.M., Scorilas A., Diamandis E.P.;			
RA : "Molecular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene.";			
RT : Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RL : [3]	SEQUENCE FROM N.A.		
RP : MEDLINE=2051030; PubMed=11054574;			
RA : Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepke B., Wang K.;			
RT : "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13. region.";			
RL : Gene 257:119-130 (2000).			
RN : [4]	SEQUENCE FROM N.A.		
RP : MEDLINE=95314630; PubMed=7794273;			
RA : Hansson L., Backman A., Ny A., Edlund M., Edholm B., Tornell J., Wallbrandt P., Egeirud T.;			
RT : "Primary substrate specificity of recombinant human stratum corneum chymotryptic enzyme.";			
RT : "Primary substrate specificity of recombinant human stratum corneum chymotryptic enzyme.";			
RA : Skyy A., Stroemqvist M., Egeirud T.;			
RT : Biochem. Biophys. Res. Commun. 21:1586-589 (1995).			
RL : [-] FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the P1 position. SCCE			
CC : CC			
CC : CC			
CC : CC			

DR EMBL; ALA45064; CAC11503.1; -.
 DR HAMAP; MF_0280; -; 1.
 DR InterPro; IPR001790; Ribosomal_L10_I.
 DR Pfam; PF00466; Ribosomal_L10_I.
 DR Ribosomal Protein; Complete Proteome.
 SQ SEQUENCE 314 AA; 34583 MW; F4D0D48680E0B6EB CRC64;
 Query Match 78.6%; Score 33; DB 1; Length 314;
 Best Local Similarity 87.5%; Pred. No. 5.5; 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; Indels 0;
 Qy 1 QRIKASKS 8
 Db 17 QRIKASRS 24

RESULT 4
 KAIN_HUMAN STANDARD; PRT; 427 AA.
 ID P96222; O9FB25;
 AC P29622; O9FB25;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4).
 OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=9403294; PubMed=8227002;
 RX Chai K.X., Chen L.-M., Chao L.;
 RT "Kallistatin: a novel human serine proteinase inhibitor. Molecular
 cloning, tissue distribution, and expression in Escherichia coli.";
 RT cloning, tissue distribution, and expression in Escherichia coli.;
 RL J. Biol. Chem. 268:24498-24505 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=95137583; PubMed=7835886;
 RX Chai K.X., Ward D.C., Chao J.J., Chao L.;
 RT "Molecular cloning, sequence analysis, and chromosomal localization
 of the human protease inhibitor 4 (kallistatin) gene (PI4)." ;
 RL Genomics 23:370-378 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 TISSUE=colon;
 MEDLINE=22382257; PubMed=11477932;
 RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Matsunaga K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casarini T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzertne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Kettman M., Madan A., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 388-403.
 RC TISSUE=Plasma;
 RX MEDLINE=9310004; PubMed=1334488;
 RA Zhou G.X., Chao L., Chao J.,
 RT "Kallistatin: a novel human tissue kallikrein inhibitor.

RT Purification, characterization, and reactive center sequence." ;
 BL J. Biol. Chem. 267:25873-25880 (1992).
 RN [5]
 RP CARBOHYDRATE-LINKAGE SITE ASN-157.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
 RT hydrazide chemistry, stable isotope labeling and mass spectrometry." ;
 RL Nat. Biotechnol. 21:660-666 (2003).
 CC -1- FUNCTION: INHIBITS HUMAN AMYLOIDYTIC AND KINININ-GENASE ACTIVITIES OF
 CC HUMAN TISSUE KALLIKREIN. INHIBITION IS ACHIEVED BY FORMATION OF AN
 CC EQUIIMOLAR, HEAT- AND SDS-SPABLE COMPLEX BETWEEN THE INHIBITOR AND
 CC THE ENZYME AND GENERATION OF A SMALL C-TERMINAL FRAGMENT OF THE
 CC INHIBITOR DUE TO CLEAVAGE AT THE REACTIVE SITE BY TISSUE
 CC KALLIKREIN.
 CC 1-1 SUBUNIT, MONOMER AND SOME HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- MISCELLANEOUS: HEPARIN BLOCKS KALLISTATIN'S COMPLEX FORMATION WITH
 CC TISSUE KALLIKREIN AND ABOLISHES ITS INHIBITORY EFFECT ON TISSUE
 CC KALLIKREIN'S ACTIVITY.
 CC -1- SIMILARITY: Belongs to the serpin family.
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 CC
 DR EMBL; L19684; AAA9454.1; -.
 DR EMBL; L28101; AAC1705.1; -.
 DR EMBL; BC014922; AAH14992.1; -.
 DR PIR; A49518; A49518.
 DR HSSP; P05154; 1; PAI.
 DR Genew; HGNC: 9948; SERPTINA4.
 DR MIM; 147935; -.
 DR CO; GO:0005515; F-protein binding; TAS.
 DR GO; GO:0004868; F-isoprin; TAS.
 DR InterPro; IPR00215; Serpin.
 DR Pfam; PF00079; serpin_1.
 DR SMART; SM0093; SERPIN_1.
 DR PROSITE; PS00384; SERPIN_1.
 DR PROSITE; PS00384; SERPIN_1.
 KW Serpin; Serine protease inhibitor; Plasma; Glycoprotein; Signal.
 PT SIGNAL; 1 20 POTENTIAL.
 PT SIGNAL; 1 20 KALLISTATIN.
 FT CHAIN 21 427
 FT ACT SITE 388 389 (POTENTIAL).
 FT CAREHYD 33 33 (POTENTIAL).
 FT CARBHYD 108 108 (POTENTIAL).
 FT CARBHYD 157 157 (POTENTIAL).
 FT CARBHYD 238 238 (POTENTIAL).
 FT CONFLICT 382 382 T->S (IN REF. 3).
 SQ SEQUENCE 427 AA; 48556 MW; 3DBBEAF956D4DAC CRC64;
 Query Match 78.6%; Score 33; DB 1; Length 427;
 Best Local Similarity 66.7%; Pred. No. 7.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 Db 355 QKLEAKSKF 363

RESULT 5
 RL10_MYCPE STANDARD; PRT; 161 AA.
 ID RL10_MYCPE
 AC Q8EVJO;
 DT 10-Oct-2003 (Rel. 42, Created)
 DT 10-Oct-2003 (Rel. 42, Last sequence update)
 DT 10-Oct-2003 (Rel. 42, Last annotation update)
 DE 50S ribosomal protein L10.

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GN BET1 OR SLY12 OR YIL04C OR YAA4C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN SEQUENCE FROM N.A.
RN [1] RP MEDLINE=9111725; PubMed=1990290;
RX Dascher C., Ossig R., Gallwitz D., Schmitt H.D.;
RA "Identification and structure of four yeast genes (SLY) that are able
RT to suppress the functional loss of YPT1, a member of the RAS
RT superfamily.";
RT Mol. Cell. Biol. 11:872-885 (1991).
RN [2] RP MEDLINE=9010955; PubMed=1396511;
RX NEWMAN A.P., GROESCH M.E.; Ferro-Novick S.;
RA "Bos1p, a membrane protein required for ER to Golgi transport in
RT yeast, co-purifies with the carrier vesicles and with Sec1p and the
RT ER membrane.";
RT EMBO J. 11:3609-3617 (1992).
RN [3] RP MEDLINE=95282515; PubMed=7762303;
RX Voss H., Tamames J., Teodoro C., Valencia A., Sensen C., Wiemann S.,
RA Schwager C., Zimmermann J., Sander C., Ansorge W.,
RA "Nucleotide sequence and analysis of the centromeric region of yeast
RT chromosome IX.";
RT Nature 387:84-87 (1997).
RN [4] RP MEDLINE=97313265; PubMed=9169870;
RX Churcher C.M., Bowman S., Baddock K., Bankier A., Brown D., Brown N.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.B., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RA "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IX.";
RT Nature 387:84-87 (1997).
CC -!- FUNCTION: Required for vesicular transport from the ER to the
CC Golgi complex. Functions as a SNARE associated with ER-derived
CC vesicles.
CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the BERTI family.
CC -!- SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.

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CC DR EMBL: Z38113; CAA86247.1; -.
CC DR EMBL: X54237; CAA38143.1; -.
CC DR EMBL: X79443; CAB38096.1; -.
CC DR PIR: C39610; C39610. -.
CC DR SGD: S000266; BET1.
CC GO: GO:000138; C:COPII-coated vesicle; IDA.
CC GO: GO:005789; C:endoplasmic reticulum membrane; IDA.
CC GO: GO:0005485; F:V-SNARE activity; IMP.
CC GO: GO:006888; P:ER to Golgi transport; IMP.
CC GO: GO:006890; P:retrograde (Golgi to ER) transport; IDA.
CC DR InterPro: IPR00739; t-SNARE; 1.
CC DR SMART: SM00397; t-SNARE; 1.
CC PROSITE: PS50192; _T-SNARE; 1.
CC DR Transport; Protein transport; Endoplasmic reticulum; Golgi stack;
KW Transmembrane; Coiled coil.

RESULT 11						
YB3C_SCHPO						
ID	YB3C_SCHPO	STANDARD;	PRT;	517 AA.		
AC	QI4342;					
DT	15-JUL-1998	(Rel. 36, Created)				
DT	15-JUL-1998	(Rel. 36, Last sequence update)				
DT	28-FEB-2003	(Rel. 41, Last annotation update)				
DB	Hypothetical protein C2F12.12c in chromosome II.					
GN	SPEC2F12.12c.					
OS	Schizosaccharomyces pombe (Fission Yeast).					
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;					
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;					
OC	Schizosaccharomyces.					
OX	NCBI_TAXID=4896;					
RN	[.]					
SEQUENCE FROM N.A.						
RP	STRAIN=N72;					
RC	MEDLINE=21848401; PubMed=11859360;					
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart					
RA	Sgouros J., Peat N., Hayles J., Baker S., Baker D., Bowman S.,					
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,					
RA	Collins M., Connor R., Conlon A., Davis P., Feltwell T., Fraser					
RA	Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodson G.,					
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels					
RA	Jones K., Jones L., Jones M., Leathem S., McDonald S., McLean J.,					
RA	Mooney P., Moule S., Munagala K., Murphy L., Niblett D., Odeil C.,					
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitzsch E.,					
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,					
RA	Shuter J., Simmonds M., Squares R., Squares S., Stevens K.,					
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead					
RA	Vanckaert G., Aert R., Robben J., Grymonpre B.,					
RA	Weitjens I., Voets E., Rieger M., Schaerer M., Mueller-Auer					
RA	Gabel C., Fuchs M., Fritz C., Holter E., Moestl D., Hilbert H.,					
RA	Borzyk K., Janger I., Beck A., Lehman H., Reinhardt R., Pohl T.M.,					
RA	Egry P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,					
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Ine laire V., Mortier S.,					
RA	Galibert P., Avres S.J., Xiang Z., Hunt C., Moore G., Hurst S.M.,					
RA	Lucas M., Rochet M., Gailhard C., Tallada V.A., Garzon A., Thoo					
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benitez					
RA	Dominguez A., Revuelta J.I., Moreno S., Armstrong J., Forsburg S.,					
RA	Cerrutti L., Lowe T., McCombie W.R., Paulsen J., Potashkin J.,					
RA	Shpakovsky G.V., Ussery D., Barrell B.G., Nurse P.;					
RT	The genome sequence of Schizosaccharomyces pombe.					
RL	Nature 415:871-880 (2002).					
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CC	ENBML: Z97211; CAB10159_1; -.					
DR	PIR: TI0129; T40129.					
DR	GeneDB: SPombe; SPBC2F12.12c; -.					
DR	Hypothetical protein.					

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OM protein - protein search, using sw model

Run on: March 1, 2004, 17:20:41 ; Search time: 30.3333 Seconds
 (without alignments)
 93.615 Million cell updates/sec

Title: US-09-905-083-99
 Perfect score: 42
 Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_25:
 1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_ncbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archeap:*

17 31 73.8 254 17 O975X7 sulfolobus
 Q8nn1 homo sapien
 Q8nt6 schizosaccharomyces pombe
 Q9bhq2 campylobacter
 Q8ta05 acrasis ros
 Q8ppv7 xanthomonas
 Q8p4t1 xanthomonas
 Q8i8k8 homo sapien
 Q7v17 penaeus vannamei
 Q8vrx1 ralstonia sphaeroides
 Q8al15 pyrococcus pseudomonas
 Q88rj0 pseudomonas
 Q84847 chlamydial
 Q8i8l6 bacillus anatum
 Q8ie81 dictyostelia
 Q86k10 dictyostelia
 Q8pd65 clostridium
 Q9fm25 arabidopsis thaliana
 Q823e3 chlamydophila
 Q8ie96 plasmidium
 Q924x2 listeria in
 Q86k80 dictyostelia
 Q8pd65 clostridium
 Q9fm25 arabidopsis
 Q93ps5 arabidopsis thaliana
 Q8cd22 mus musculus
 Q96845 caenorhabditis elegans
 Q18372 caenorhabditis
 Q87bb1 xylorella fass
 Q86l00 dictyostelia

ALIGNMENTS

RESULT 1

Q8NPFV7 ID Q8NPFV7 PRELIMINARY; PRT; 181 AA.
 AC Q8NPFV7; DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

DE Kallikrein 7 short variant protein.
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 OC NCBI_TAXID=9606.

RN [1] SEQUENCE FROM N.A.
 RC TISSUE-Ovarian carcinoma;
 RA Dong Y., Kaushal A., Clements J.A.;
 RT "Human Kellikrein 7 (KLK7)" short variant mRNA from ovarian carcinoma".
 RL Submitted AUG-2001 to the EMBL/GenBank/DBJ databases.
 CC ID SIMILARITY: AAN03663.1; EMBL: AF411215; GO: GO-0004263; F: chymotrypsin activity; IEA.
 DR GO: GO-0008233; F: peptidase activity; IEA.
 DR GO: GO-0008233; F: trypsin activity; IEA.
 DR GO: GO-0005608; P: proteolysis and peptidolysis; IEA.
 DR InterPro: IPR000003; Cys_Ser_trypsin.
 DR InterPro: IPR001254; Peptidase_S1A.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS; PR0722; CHM01RYFSIN.
 DR SMART; SM00020; TRYSPIN_1.
 DR PROSITE; P50240; TRYSPIN_DOM_1.
 DR PROSITE; P801325; TRYSPIN_SER_1.
 KW Hydrolase; Protease; Serine_protease.
 SQ SEQUENCE 181 AA; 19887 MW; 86A28A03EB0C2D78 CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	181	4 Q8NPFV7	Q8nn1 homo sapien
2	42	100.0	253	4 Q8NPFV7	Q8nn19 mycoplasma pneumoniae
3	36	85.7	234	11 Q9R048	Q9R048 mus musculus
4	36	85.7	249	11 Q91VE3	Q91VE3 mus musculus
5	34	81.0	294	16 Q88Q37	Q88Q37 pseudomonas aeruginosa
6	34	81.0	683	16 Q82XB0	Q82XB0 nitrosoomonas
7	33	78.6	445	4 Q86TR9	Q86TR9 homo sapien
8	33	78.6	671	16 Q8EUP9	Q8EUP9
9	32	76.2	274	5 Q9U0Z3	Q9U0Z3 leishmania
10	32	76.2	467	5 Q8IBN4	Q8IBN4 plasmidium
11	32	76.2	474	16 Q7VRX5	Q7VRX5 candidatus
12	32	76.2	490	10 Q8SAQ5	Q8SAQ5 chlamydomon
13	32	76.2	684	5 Q816K2	Q816K2 holotrichia
14	32	76.2	895	17 Q9YAU1	Q9YAU1 homo sapien
15	31	73.8	177	4 Q8TB05	Q8TB05 sphingomona
16	31	73.8	248	2 Q937X0	Q937X0 sphingomona

Query Match 100.0%; Score 42; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR	EMBL; BC027823; AAH27823..1;	Qy	1 QRIKAKSF 9
DR	EMBL; AK029477; BAC26667..1;	Db	259 QRIKAKSF 267
DR	HSSP; P00761; IANL..		
DR	MGID; MG16336..		
DR	GO; GO:004463; P:chymotrypsin activity; IEA.		
DR	GO; GO:008833; P:Peptidase activity; IEA.		
DR	GO; GO:004215; P:trypsin activity; IEA.		
DR	GO; GO:006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR009090; Cys_Ser_trypsin.		
DR	InterPro; IPR001254; Peptidase_S1.		
DR	InterPro; IPR001314; Peptidase_S1A.		
PFam;	PF00089; trypsin; 1.		
PRINTS;	PR0072; CHYMOTRYPSIN.		
DR	PROSITE; PS02420; TRYPSIN DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN HIS; 1.		
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
RW	Hydrolase; Protease; Serine Protease.		
SQ	SEQUENCE: 249 AA; 27257 MW; 0D4E380F12D14F87 CRC64;	OX	
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RC	STRAIN=ATCC 19718 / IFO 14298;
		MDLINE=22586410; PubMed=12700255;	
		RA	Chain P.; Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
		RA	Hauser L., Hooper A.B., Klotz M.G., Sayavedra-Soto L.A.,
		RA	Archer D.M., Hommes N.G., Whittaker M.M., ARP D.J.;
		RT	"Complete genome sequence of the ammonia-oxidizing bacterium and
		RT	obligate chemolithoautotroph Nitrosomas europaea.";
		RL	J. Bacteriol. 185:2759-2773(2003).
		DR	EMBL; BX321857; CAD84288 1..
		DR	GO; GO:0016020; F:ATP binding; IEA.
		DR	GO; GO:0016301; F:kinase activity; IEA.
		DR	GO; GO:000115; P:two-component sensor molecule activity; IEA.
		DR	GO; GO:0007165; P:signal transduction; IEA.
		DR	InterPro; IP0003594; ATPbind_Atpase.
		DR	InterPro; IP0004358; Bact_sens_Dr_C.
		DR	InterPro; IP0005467; His_Kinase.
		DR	InterPro; IP0003651; His_Kinase_N.
		DR	Pfam; PF02518; HATPase_C..1.
		DR	Pfam; PP0510..; HISKA_1..
		DR	PRINTS; PR00344; BCTRSENSOR.
		DR	SMART; SM00387; HATPase_C..1.
		DR	PROSITE; PS50109; HIS_KIN..1..
		KW	Kinase; Complete proteome.
		SEQUENCE	683 AA; 77013 MW; 6989B95EB6543ED4 CRC64;
		SQ	Query Match 81.0%; Score 34; DB 16; Length 683;
			Best Local Similarity 88.9%; Prod. No. 62;
			Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
		Qy	1 QRIKAKSF 9
		Db	548 QRIKAKSF 556
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RC	TISSUE=Fetal liver;
		RA	Genoscope;

RESULT 14

Q9YAU1	PRELIMINARY;	PRT;	895 AA.
ID	Q9YAU1;		
AC			
DT	01-NOV-1999 (TREMBREL; 12, Created)		
DT	01-NOV-1999 (TREMBREL; 12, Last sequence update)		
DT	01-OCT-2003 (TREMBREL; 25, Last annotation update)		
DE	895AA long hypothetical DNA-directed RNA polymerase subunit A'.		
GN	APE1853.		
OS	Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;		
OC	Desulfurococcaceae; Aeropyrum.		
OX	NCBI_TaxID=566336;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=KL;		
RX	MEDLINE=9310339; PubMed=10382966;		
RA	Kawarabayasi S., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,		
RA	Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankei A., Kosugi H.,		
RA	Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,		
RA	Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,		
RA	Yamazaki J., Kushida N., Ochiai A., Aoki K.-I., Kubota K.,		
RA	Nakamura Y., Nomura N., Sako Y., Kikuchi H.,		
RT	"Complete genome sequence of an aerobic hyper-thermophilic		
RT	archaeon, <i>Aeropyrum pernix</i> K1."		
RL	DNA Res. 6:83-101(1999).		
DR	EMBL; AP00062; BAB80857.1; -.		
DR	PIR; D72571; D72571.		
DR	GO:0005634; C-nucleus; IEA.		
DR	GO:0003677; F-DNA binding; IEA.		
DR	GO:0003899; F-DNA-directed RNA polymerase activity; IEA.		
DR	GO:0006350; P-transcription; IEA.		
DR	InterPro; IPR006592; RNA_Po1_N.		
DR	InterPro; IPR007072; RNA_Po1_K.		
DR	InterPro; IPR007080; RNA_Po1_Rpb1_1.		
DR	InterPro; IPR007066; RNA_Po1_Rpb1_1.		
DR	InterPro; IPR007083; RNA_Po1_Rpb1_4.		
DR	InterPro; IPR007081; RNA_Po1_Rpb1_5.		
DR	Pfam; PF04997; RNA_Po1_Rpb1_1.		
DR	Pfam; PF00623; RNA_Po1_Rpb1_2;		
DR	Pfam; PF04993; RNA_Po1_Rpb1_3;		
DR	Pfam; PF00000; RNA_Po1_Rpb1_4;		
DR	Pfam; PF04998; RNA_Po1_Rpb1_5;		
DR	SMART; SM00663; RPOA_N_1.		
KW	DNA-directed RNA polymerase; Complete Proteome.		
SQ	SEQUENCE 895 AA; 101740 MW; 1E01BCC6B4BD0AAE CRC64;		

Query Match Score 76.2%; Pred. No. 2.3e+02; Length 895;

Best Local Similarity 75.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKS 8

Db 885 QRVKASKA 832

RESULT 15

Q8TB05	PRELIMINARY;	PRT;	177 AA.
ID	Q8TB05		
AC	Q8TB05;		
DT	01-JUN-2002 (T-EMBLrel. 21, Created)		
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Similar to LOC146557.		
OS	<i>Homo sapiens</i> (Human).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Skin;		
RA	Strauberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.		
RL			